

STIC-Biotech/ChemLib

131534

From: Hutzell, Paula  
Sent: Wednesday, September 01, 2004 3:39 PM  
To: Graser, Jennifer; STIC-Biotech/ChemLib  
Subject: RE: rush search

approved

-----Original Message-----

From: Graser, Jennifer  
Sent: Wednesday, September 01, 2004 3:13 PM  
To: Hutzell, Paula  
Subject: rush search  
Importance: High

Hi Paula,  
Could you please authorize this rush search for an Election?  
Thanks, Jennifer

-----  
STIC:

Please search jnucleotides 918-1580 of SEQ ID NO: 12 from 10/625,221 in  
pending and commercial databases.

Thanks,  
Jennifer Graser  
REM 3B09 (mailbox 3C18)  
Art Unit 1645  
272-0858

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 17:15:56 ; Search time 2409 Seconds  
(without alignments)  
8218.608 Million cell updates/sec

Title: US-10-625-221-12\_COPY\_918\_1580

Perfect score: 663

Sequence: 1 caacaagaccgacccaag.....aagttacctaacaaccaag 663

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_pln:\*

19: em\_gss\_vrt:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrt:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78.8	11.9	1101	29	CNS00EVL
C 2	77.4	11.7	1101	29	CNS0039G
C 3	72.8	11.0	994	13	AX414650
C 4	72.4	10.9	1201	29	CNS0167M

C 5	71.4	10.8	821	29	CNS0090X
C 6	69.6	10.5	1101	29	CNS001FB
C 7	69.4	10.5	1201	9	AL565455
C 8	68.6	10.3	1056	13	AX415058
C 9	68	10.3	1201	9	AL536104
C 10	67.6	10.2	840	29	CNS06V50
C 11	67.6	10.2	1201	9	AL536104
C 12	66.6	10.0	1201	13	AX439779
C 13	66	10.0	1200	13	AX437739
C 14	65.8	9.9	945	29	CNS04D0K
C 15	65.8	9.9	1101	29	CNS0039G
C 16	65.6	9.9	999	13	AX380865
C 17	65.2	9.8	1201	13	AX364179
C 18	65	9.8	1200	13	AX436510
C 19	64.8	9.8	853	29	CG767791
C 20	64.4	9.7	759	29	CNS06QXV
C 21	64.4	9.7	1201	9	AL531981
C 22	64.2	9.7	1043	29	CNS0145P
C 23	64	9.7	1200	13	AX415878
C 24	63.6	9.6	1199	13	AX375702
C 25	63.4	9.6	1101	29	CNS008X3
C 26	63.4	9.6	1126	13	AX446388
C 27	63.4	9.6	1200	13	AX415878
C 28	63.2	9.5	1008	14	CD329035
C 29	63.2	9.5	1201	13	AX462660
C 30	63.2	9.5	1896	29	CG753083
C 31	63	9.5	1200	29	CNS016CO
C 32	62.8	9.5	996	29	CNS00FUH
C 33	62.6	9.4	886	28	BH177277
C 34	62.6	9.4	886	29	CNS07JUX
C 35	62.6	9.4	1101	29	CNS0039L
C 36	62.6	9.4	1318	29	CG752308
C 37	62.4	9.4	1201	9	AL532464
C 38	62.2	9.4	1165	13	AX338369
C 39	62.2	9.4	1200	13	AX437758
C 40	62	9.4	986	13	AX366417
C 41	62	9.4	1064	13	AX361825
C 42	62	9.4	1101	29	CNS017V2
C 43	62	9.4	1169	29	CNS06RHQ
C 44	61.8	9.3	932	9	AL514901
C 45	61.8	9.3	1001	29	CNS0155H

#### ALIGNMENTS

RESULT 1	CNS00EVL	1101 bp	DNA	linear	GSS 04-JUN-1999
LOCUS	CNS00EVL				
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL069706				
VERSION	AL069706.1				GI:4949849
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1 (bases 1 to 1101)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitfly.org">http://www.fruitfly.org</a> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosier in Pieter de Jong's laboratory in the Department of				

RESULT 2  
CNS0039G/c  
LOCUS  
DEFINITION  
CNS0039G 1101 bp DNA linear GSS 03-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR0BK10 of RPEC1-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

8 TTGAAACAAATAAAAAA  
:::|:::|:::|  
6 ADRDWAKARAWRARRDRA  
8 TTACAGATAATAAGCAAC  
|:|:

8 TTGAAACRAATAA AAAAATGTGA CTGCTCAAGAAATTG ACATTAAGA GTTAGAAAATATC 457  
::: : : : : : : : : : : : : : : : : :  
6 ADRDWA KARAWEAR DRA--RAARD RRTTKGKT TTTATWTTWA ARAAWAWATTTA 539  
: : : : : : : : : : : : : : : : : :  
8 TTACAGATAATPA GCAACTATAT ATACTATG AACCTTCAA ATATGAA ACTGGATATATA 517  
: : : : : : : : : : : : : : : : : :

















QY 504 AACTGGATATATAAGTTTCATACCTAAGATAAAGAAAGTTT 546  
 Db 903 TATAAAAAAAAAAAAAAAAAATTTTAAAAAATAAAAAAATAT 945

RESULT 15  
 CNS0039G 1101 bp DNA linear GSS 03-JUN-1999  
 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #  
 DEFINITION BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 ACCESSION AL063921  
 VERSION 1  
 KEYWORDS AL063921.1 GI:4941778  
 SOURCE GSS.  
 ORGANISM Drosophila melanogaster (fruit fly)  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 1101)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mamoser in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
 p1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
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 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone="BACR08K10"  
 /clone\_lib="RPCI-98"  
 /note="end : TET3"

ORIGIN  
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 Best Local Similarity 21.9%; Pred. No. 0.0083;  
 Matches 115; Conservative 198; Mismatches 211; Indels 1; Gaps 1;  
 QY 138 AATATATATGTTTCAGGGCCAAATATGATAAATTAATAAAGTAAAGAACCAAGA 197  
 Db 395 MATATATAAATTTTATTAATAAATAAATAATTTAAATAAATAAATAATTTAAATAA 454  
 QY 198 GATGGCACTTATTATTAAGGATAAAGACCTTGATATTATGTTGATAGATATACCATCT 257  
 Db 455 AAWATAATTTTAAATTAATAAATAAATAATTTTATTTTATTTTATTTTATTTTATTTT 514  
 QY 258 CTGTTATTATTTGTAAGATGCAGAGGAGTGCATGATCTACGGAGGGGTAAACATCA 317  
 Db 515 AAWAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 574  
 QY 318 TGAAGGGAATCATTTAGAATTCCTAAAAAGATAGCTGTTAAAGTATCATCATCGATGAT 377  
 Db 575 YTTTYYHYTY 633  
 QY 378 CCAAGCCATCATTTGATATGAAACAAATTAATAAATAAATAAATAAATAAATAAATAA 437

Db 634 TTTAAYYYTCTMYYYHYHWHHHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHA 693  
 QY 438 CTATAAAGCTTAGAAAAATATCTTACAGATAAATAAGCAACTATATATACTATGACCTTCTAA 497  
 Db 694 CTTCTCHCYYYHYHHTAHTHTTHHWAHYHYHYHYHYHYHYHYHYHYHYHYHYHYHYHY 753  
 QY 498 ATATGAAACTGGATATATAAAGTTTCATACCTAAGATAAAGAAAGTATTTTGGTTTGTATTT 557  
 Db 754 HTTWAWAHAMMMHHAHYAAAAAATAATTHVHHTTHYMHHTYMYHYHYMYTCCYMCY 813  
 QY 558 TTTCCCTGAACACAGATTTTACTCAATCTAAATATCTTATGATATATAAGATAAAGAAC 617  
 Db 814 HCWHYYTATYTCWTWHEHMTWTHYHHTTWHMMHTTTHWAWHHTTTCWMMWHHTTWTWA 873  
 QY 618 GCTTGACTCAACACACAGCCAAATTTGAAGTCTTACCTAACAACCAA 662  
 Db 874 THCWACMTHHWHHWHHMH 918

Search completed: September 3, 2004, 18:56:46  
 Job time : 2413 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 17:19:26 ; Search time 77 Seconds  
(without alignments)  
4778.343 Million cell updates/sec

Title: US-10-625-221-12\_COPY\_918\_1580  
Perfect score: 663  
Sequence: 1 caacaagaccgcgacccaag.....aagtcactaaccaaccaag 663

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA.\*  
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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	1851	4	US-08-973-391C-12
2	661.4	99.8	1837	2	US-08-743-637B-33
3	661.4	99.8	1837	3	US-08-526-840B-33
4	658.2	99.3	1837	4	US-09-144-776B-15
5	166.8	25.2	773	1	US-08-446-918A-1
6	166.8	25.2	773	2	US-08-580-806-1
7	166.8	25.2	773	4	US-08-144-776B-5
8	164.2	24.8	1095	4	US-09-144-776B-13
9	158.8	24.0	723	4	US-09-350-755A-3
10	158.8	24.0	801	4	US-09-350-755A-2
11	158.8	24.0	1388	4	US-09-144-776B-9
12	158.8	24.0	1712	4	US-09-144-776B-7
13	112	16.9	815	4	US-09-414-276-7
14	71	10.7	757	4	US-09-144-776B-3
15	71	10.7	757	4	US-09-350-755A-1
16	71	10.7	830	4	US-09-144-776B-1
17	66.2	10.0	675	4	US-08-956-171E-887
18	62.2	9.4	1789	4	US-08-936-165A-116
19	59	8.9	751	1	US-08-446-918A-3
20	59	8.9	751	2	US-08-580-806-3
21	52.4	7.9	640681	4	US-09-790-988-1
22	50.8	7.7	19124	2	US-08-487-826B-13
23	48.6	7.3	1664976	4	US-08-916-421B-1
C 24	48.4	7.3	4185	4	US-09-417-485D-7
C 25	48.4	7.3	10640	4	US-09-417-485D-5
C 26	47.6	7.2	1887	4	US-09-601-198-39
C 27	47.6	7.2	640681	4	US-09-790-988-1

C 28	47	7.1	53332	4	US-09-801-861-3	Sequence 3, Appli
C 29	46.8	7.1	1374	4	US-09-601-198-158	Sequence 158, App
C 30	46.8	7.1	7218	1	US-08-232-463-14	Sequence 14, Appl
C 31	46.8	7.1	10467	4	US-10-204-708-2	Sequence 2, Appli
C 32	46.4	7.0	665	2	US-08-883-785A-36	Sequence 36, Appl
C 33	46.4	7.0	1851	4	US-09-601-198-51	Sequence 51, Appl
C 34	46.2	7.0	660	1	US-07-991-867B-32	Sequence 32, Appl
C 35	46.2	7.0	660	2	US-08-107-755A-32	Sequence 32, Appl
C 36	46.2	7.0	660	1	US-08-544-332-32	Sequence 32, Appl
C 37	46.2	7.0	660	4	US-09-370-861A-32	Sequence 32, Appl
C 38	46.2	7.0	1511	1	US-07-991-867B-8	Sequence 8, Appli
C 39	46.2	7.0	1511	1	US-08-107-755A-8	Sequence 8, Appli
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C 42	46.2	7.0	4810	3	US-08-852-629-11	Sequence 11, Appl
C 43	46.2	7.0	4838	3	US-08-852-629-15	Sequence 15, Appl
C 44	45	6.8	5152	4	US-10-204-708-73	Sequence 73, Appl
C 45	45	6.8	11015	4	US-10-204-708-55	Sequence 55, Appl

#### ALIGNMENTS

RESULT 1  
US-08-973-391C-12  
; Sequence 12, Application US/08973391C  
; Patent No. 6632441  
; GENERAL INFORMATION:  
; APPLICANT: Schlievert, Patrick M.  
; APPLICANT: Rosigiani, Manuela  
; APPLICANT: Stoeher, Jennifer  
; APPLICANT: Ohlendorf, Douglas  
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE  
; FILE REFERENCE: 600.311USWO  
; CURRENT APPLICATION NUMBER: US/08/973,391C  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: PCT/US96/10252  
; PRIOR FILING DATE: 1996-06-07  
; PRIOR APPLICATION NUMBER: US 08/480,261  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 1851  
; TYPE: DNA  
; ORGANISM: Streptococcus pyogenes  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (828)..(1583)  
; OTHER INFORMATION:  
US-08-973-391C-12

Qy	1	CAACAAGACCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAGTAAACCTTCAAAAT	60
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Qy	61	ATATATTTCTTTATGAGGTGACCTGTACTACAGAGATGTGAATCTGTGTATCAA	120
Db	978	ATATATTTCTTTATGAGGTGACCTGTACTACAGAGATGTGAATCTGTGTATCAA	1037
Qy	121	CTTTTATCTCACCATTATATATATATGTTTTCAGGGCCAAATATGATAAATAAACAAT	180
Db	1038	CTTTTATCTCACCATTATATATATGTTTTCAGGGCCAAATATGATAAATAAACAAT	1097
Qy	181	GAACCTTAAGAACCAAGAGATGGCAACTTTATTTTAAAGATAAAACGTTGATATTTGGT	240
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Db 1158 GTAGATATACCTCTCTGTTATTTATGTAATGCGAAGAGAGTGCATGTATCTAC 1217  
QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAAAGATAGCTGTTAAA 360  
Db 1218 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAAAGATAGCTGTTAAA 1277  
QY 361 GTATCAATCGATGGTATCCAAAGCCTATCAITTTGATATTAAGCAAAATAAAAAATGGTA 420  
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QY 601 TATAAGATAATGAAGCGCTTGACTCAAAACACAGCCAAATTTGAAGTCTTACCTAAACACC 660  
Db 1518 TATAAGATAATGAAGCGCTTGACTCAAAACACAGCCAAATTTGAAGTCTTACCTAAACACC 1577  
QY 661 AAG 663  
Db 1578 AAG 1580

## RESULT 2

US-08-743-637B-33  
; Sequence 33, Application US/08743637B  
; Patent No. 5994066

## GENERAL INFORMATION:

; APPLICANT: BERGERON, Michel G.  
; APPLICANT: PICARD, Francois J.  
; APPLICANT: OUELLETTE, Marc  
; APPLICANT: ROY, Paul H.  
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA  
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND  
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED  
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...  
; NUMBER OF SEQUENCES: 273  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: QUARLES & BRADY  
; STREET: 411 EAST WISCONSIN AVENUE  
; CITY: MILWAUKEE  
; STATE: WISCONSIN  
; COUNTRY: USA  
; ZIP: 53202-4497

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/743,637B  
; FILING DATE: 04-NOV-1996  
; CLASSIFICATION: -435

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/526,840  
; FILING DATE: 11-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BAKER, Jean C.  
; REGISTRATION NUMBER: 31433  
; REFERENCE/DOCKET NUMBER: 850586.90012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 277-5000  
; TELEFAX: (414) 277-5591  
; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1837 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pyogenes  
; US-08-743-637B-33

Query Match 99.8%; Score 661.4; DB 2; Length 1837;

Best Local Similarity 99.8%; Pred. No. 2e-143;  
Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCAGCCAACTTCAACAGATCTAGTTTGTAGTTAAAAACCTTCAAAAT 60  
Db 904 CAACAAGACCCCGATCCAGCCAACTTCAACAGATCTAGTTTGTAGTTAAAAACCTTCAAAAT 963  
QY 61 ATATATTTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGTGAATCTGTTGATCAA 120  
Db 964 ATATATTTTCTTTATGAGGGTGACCTGTTACTACGAGAAATGTGAATCTGTTGATCAA 1023  
QY 121 CTTTATCTCACCATTAAATATATATGTTTTCAGGCGCAAAATATCATATAATTAATAAAT 180  
Db 1024 CTTTATCTCACCATTAAATATATGTTTTCAGGCGCAAAATATCATATAATTAATAAAT 1083  
QY 181 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATATAAAACCTTGTATTTATGTT 240  
Db 1084 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATATAAAACCTTGTATTTATGTT 1143  
QY 241 GTAGAATATTACCATCTCTGTTTATTTATGTAAGATGCAAGAGAGTGCATGTATCTAC 300  
Db 1144 GTAGAATATTACCATCTCTGTTTATTTATGTAAGATGCAAGAGAGTGCATGTATCTAC 1203  
QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCATTTTAGAAATTCCTAAAAAGATAGCTGTTAAA 360  
Db 1204 GGAGGGGTAAACAAATCATGAAGGGAATCATTTTAGAAATTCCTAAAAAGATAGCTGTTAAA 1263  
QY 361 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTTGAACAAATAAAAAATGGTA 420  
Db 1264 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTTGAACAAATAAAAAATGGTA 1323  
QY 421 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATAAATGAAGCAACTATAT 480  
Db 1324 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATAAATGAAGCAACTATAT 1383  
QY 481 ACTAATGGACCTCTTAAATATGAAGTGGATATATAAAGTTCATACCTTAAGATAAAGAA 540  
Db 1384 ACTAATGGACCTCTTAAATATGAAGTGGATATATAAAGTTCATACCTTAAGATAAAGAA 1443  
QY 541 AGTTTTTGGTTGATTTTTCCTGAACAGAGATTTTACTCAATCTAAATATCTTATGATA 600  
Db 1444 AGTTTTTGGTTGATTTTTCCTGAACAGAGATTTTACTCAATCTAAATATCTTATGATA 1503  
QY 601 TATAAGATAAATGAAGCGTTGACTCAAAACACAGCCAAATTTGAAGTCTTACCTAAACACC 660  
Db 1504 TATAAGATAAATGAAGCGTTGACTCAAAACACAGCCAAATTTGAAGTCTTACCTAAACACC 1563  
QY 661 AAG 663  
Db 1564 AAG 1566

## RESULT 3

US-08-526-840B-33  
; Sequence 33, Application US/08526840B  
; Patent No. 6001564

## GENERAL INFORMATION:

; APPLICANT: BERGERON, Michel G.  
; APPLICANT: OUELLETTE, Marc  
; APPLICANT: ROY, Paul H.  
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND  
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY

TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES  
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...

NUMBER OF SEQUENCES: 177

CORRESPONDENCE ADDRESS:

ADDRESSEE: QUARLES & BRADY

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: USA

ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

PATENTIN RELEASE #1.0, Version #1.30

APPLICATION NUMBER: US/08/526,840B

FILING DATE: 11-SEP-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/304,732

FILING DATE: 12-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 850586.90012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 277-5000

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 1837 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORGANISM: Streptococcus pyogenes

US-08-526-840B-33

Query Match 99.8%; Score 661.4; DB 3; Length 1837;

Best Local Similarity 99.8%; Pred. No. 2e-143;

Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAACAAGACCCGATCCCAAGCACTTACAGATCTAGTTAGTATATAAAACCTTCAAAAT 60

DB 904 CAACAAGACCCGATCCCAAGCACTTACAGATCTAGTTAGTATATAAAACCTTCAAAAT 963

QY 61 ATATATTTCTTTATGAGGGTGACCTGTTACTCAGAGATGTGAAATCTGTTGATCAA 120

DB 964 ATATATTTCTTTATGAGGGTGACCTGTTACTCAGAGATGTGAAATCTGTTGATCAA 1023

QY 121 TTTTATCTCACTTAAATATAAATGTTTTCAGGGCCAAATTTATGATAATTAATAAACT 180

DB 1024 CTTTATCTCACTTAAATATAAATGTTTTCAGGGCCAAATTTATGATAATTAATAAACT 1083

QY 181 GAACCTTAAGACCAAGATGCGACCTTATTTAAGATTAAGATTAAGATTAAGATTAAGAT 240

DB 1084 GAACCTTAAGACCAAGATGCGACCTTATTTAAGATTAAGATTAAGATTAAGATTAAGAT 1143

QY 241 GTAGAATATTACCATCTCTGTTATTTATGTAATGCAAGAGAGTGCATGATCTAC 300

DB 1144 GTAGAATATTACCATCTCTGTTATTTATGTAATGCAAGAGAGTGCATGATCTAC 1203

QY 301 GGAGGGGTAAACAATCATGAAGGGAATCATTTAGAAATTCCTTAAAGATAGTCTGTTAAA 360

DB 1204 GGAGGGGTAAACAATCATGAAGGGAATCATTTAGAAATTCCTTAAAGATAGTCTGTTAAA 1263

QY 361 GTATCAATCGATGGTATCCAAAGCCATCTTTCATATTGAAACAATATAAAATAGGTA 420

DB 1264 GTATCAATCGATGGTATCCAAAGCCATCTTTCATATTGAAACAATATAAAATAGGTA 1323

QY 421 ACTGCTCAAGATTAAGATATAAAGTTAGAAAATCTTACAGATAATAAGCAACTATAT 480

DB 1324 ACTGCTCAAGATTAAGATATAAAGTTAGAAAATCTTACAGATAATAAGCAACTATAT 1383

QY 481 ACTAATGGACCTTCTAAATATGAACCTGGATATATAAAGTTTCATACCTTAAGATAAGAA 540

DB 1384 ACTAATGGACCTTCTAAATATGAACCTGGATATATAAAGTTTCATACCTTAAGATAAGAA 1443

QY 541 AGTTTTGGTTTGATTTTTTCCCTGGAACCAAGATTTACTCAATCTAATATCTTATGATA 600

DB 1444 AGTTTTGGTTTGATTTTTTCCCTGGAACCAAGATTTACTCAATCTAATATCTTATGATA 1503

QY 601 TATAAGATTAATGAACCTGTTGACTCAACACAGCCAAATTTGAAGTCTACTTACCAACC 660

DB 1504 TATAAGATTAATGAACCTGTTGACTCAACACAGCCAAATTTGAAGTCTACTTACCAACC 1563

QY 661 AAG 663

DB 1564 AAG 1566

RESULT 4

US-09-144-776B-15

; Sequence 15, Application US/09144776B

; Patent No. 6399332

; GENERAL INFORMATION:

; APPLICANT: Robert G. Ulrich,

; Mark A. Olson

; Sina Bavari

; TITLE OF INVENTION: Bacterial Superantigen

; Vaccines

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles H. Harris

; STREET: US Army MRC -504 Scott Street

; MCMR-JA (Charles H. Harris-Patent

; Atty)

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.5

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/144,776B

; FILING DATE: 01-Sep-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/882,431

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Charles H. Harris

; REGISTRATION NUMBER: 34,616

; REFERENCE/DOCKET NUMBER: <Unknown>

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 619-2065

; TELEFAX: (301) 619-7714

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1837

; TYPE: Nucleic Acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Unknown

; MOLECULE TYPE: DNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-144-776B-15

Query Match 99.3%; Score 658.2; DB 4; Length 1837;

Best Local Similarity 99.5%; Pred. No. 1.1e-142;

Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAGACCCGATCCAGCAACTTCACAGACTAGTTAGTTAAACACCTTCAAAAT 60  
DB |||||  
QY 904 CAACAGACCCGATCCAGCAACTTCACAGACTAGTTAGTTAAACACCTTCAAAAT 963  
DB |||||  
QY 61 ATATATTTCTTTATGAGGCTGACCTGTTACTCAGGAGAAATGTGAATCTCTGTCATCA 120  
DB |||||  
QY 964 ATATATTTCTTTATGAGGCTGACCTGTTACTCAGGAGAAATGTGAATCTCTGTCATCA 1023  
DB |||||  
QY 121 CTTTATCTCACCATTATATATATATGTTTCAGGGCCAAATATGATAAAATTAATAACT 180  
DB |||||  
QY 1024 CTTAGATCTCAGGATTAATATATATGTTTCAGGGCCAAATATGATAAAATTAATAACT 1083  
DB |||||  
QY 181 GAACTTAACACCAAGAGATGCAACTTTATTTAGGATAAAAGCTTGATATTTATGTT 240  
DB |||||  
QY 1084 GAACTTTAAGAACCAAGAGATGCAACTTTATTTAGGATAAAAGCTTGATATTTATGTT 1143  
DB |||||  
QY 241 GTAGAAATTTACCATCTCTGTTATTTATGTAAGAAATGCAAGAGGAGTGCATGTATCTAC 300  
DB |||||  
QY 1144 GTAGAAATTTACCATCTCTGTTATTTATGTAAGAAATGCAAGAGGAGTGCATGTATCTAC 1203  
DB |||||  
QY 301 GGAGGGGTAAACAAATCATGAGGAAATCAATTTAGAAATTCCTTAAAGATAGTCTGTTAAA 360  
DB |||||  
QY 1204 GGAGGGGTAAACAAATCATGAGGAAATCAATTTAGAAATTCCTTAAAGATAGTCTGTTAAA 1263  
DB |||||  
QY 361 GPATCAATCGATGGTATCCAAAGCCTATCATTTGATATTTGAAACAAATTAAGAAATGGTA 420  
DB |||||  
QY 1264 GPATCAATCGATGGTATCCAAAGCCTATCATTTGATATTTGAAACAAATTAAGAAATGGTA 1323  
DB |||||  
QY 421 ACTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATAAATAAGCAACTATAT 480  
DB |||||  
QY 1324 ACTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATAAATAAGCAACTATAT 1383  
DB |||||  
QY 481 ACTAATGAGACCTTAAATATGAAATGAACTGATATATAAGTTTCACTACCTTAAGATAAAGAA 540  
DB |||||  
QY 1384 ACTAATGAGACCTTAAATATGAAATGAACTGATATATAAGTTTCACTACCTTAAGATAAAGAA 1443  
DB |||||  
QY 541 AGTTTGTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATATCTTATGATA 600  
DB |||||  
QY 1444 AGTTTGTGTTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATATCTTATGATA 1503  
DB |||||  
QY 601 TATAAGATAATGAAACGTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCAACC 660  
DB |||||  
QY 1504 TATAAGATAATGAAACGTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCAACC 1563  
DB |||||  
QY 661 AAG 663  
DB 1564 AAG 1566

## RESULT 5

US-08-446-918A-1  
; Sequence 1, Application US/08446918A  
; Patent No. 5705151  
; GENERAL INFORMATION:  
; APPLICANT: Dow, Steve W.  
; APPLICANT: Elmslie, Robyn E.  
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; STREET: Sheridan Ross & McIntosh  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.A.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,918A  
; FILING DATE: 18-MAY-1995

CLASSIFICATION: 552  
ATTORNEY/AGENT INFORMATION:  
NAME: Kovarik, Joseph E.  
REGISTRATION NUMBER: 33,005  
REFERENCE/DOCKET NUMBER: 2879-29  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 773 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..768  
US-08-446-918A-1

Query Match 25.2%; Score 166.8; DB 1; Length 773;  
Best Local Similarity 59.1%; Pred. No. 9.4e-30;  
Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;

QY 56 AAAATATATATTTCTTTATGAGGGTGACCTGTTACTCACGAGAAATGTGAATCTGTG 115  
DB |||||  
QY 113 AAAATATGAAAGTTTGTATGATGATATCAATCATGATCAGCAATAAACGTTAAATCTATAG 172  
DB |||||  
QY 116 ATCAACTTTTATCTCACCATTTAATATATATATGTTTTCAGGGCCA-----AAATTATG 166  
DB |||||  
QY 173 ATCAATTTCTATCTTGTACCTTAATATATCTTATTAAGCACACTAAGTTAGGAAATATG 232  
DB |||||  
QY 167 ATAAATTAATAACTGAACTTAAGAACCAAGAGATGGCACTTTATTTAAGGATAAAACG 226  
DB |||||  
QY 233 ATAATGTTTCGATCGAATTTTAAAAACAAAGATTTAGCTCATATAATACAAAGATAAATAG 292  
DB |||||  
QY 227 TTGATATTTATGTTGTAGAAATATTAACCATCTCTGTTATTTATGTAAGAA-----275  
DB |||||  
QY 293 TAGATGTTTGGAGCTAATTAATTAATTAATCAATGTTATTTTCTAAAAAACAATGATA 352  
DB |||||  
QY 276 -----TGCAGAAAGGAGTGCATGTATCTACGAGGGGTAAACAAATCATG 319  
DB |||||  
QY 353 TTAAATTCGCATCAAACTGACAAAACGAAAACTTGATGTATGTTGTTGTTAACTGAGCATA 412  
DB |||||  
QY 320 AAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCTGTTAAAGTATCAATCGATGTTATCC 379  
DB |||||  
QY 413 ATGGAACCAATTAGATAAATATAGAGTATTACTGTTTCGGGTATTTGGAAGATGTTAAAA 472  
DB |||||  
QY 380 AAAGCCTATCATTTGATATGAAACAAATTAATAATGTTACTGCTCAAGAAATTAGACT 439  
DB |||||  
QY 473 ATTTATTTCTTTGACGTACAACTAATAGAAAAGGTGACTGCTCAGAAATTAGATT 532  
DB |||||  
QY 440 ATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATATATACTAATGACCTCTTAAT 499  
DB |||||  
QY 533 ACCTAACTCGTCACATTGTTGGTGAATAATAAAAACTCTATGAATTTAAACAACCTCGCCT 592  
DB |||||  
QY 500 ATGAACTGGATATATAAGTTTCATACCTAAGAAATAAGAAAGTTTTCGTTGATTTT 559  
DB |||||  
QY 593 ATGAAACGGATATATTAATTTATA---GAAAAAGAGAATAGCTTTTGGTATGACATGA 649  
DB |||||  
QY 560 TCCCTGAAACCCAG-----AAATTACTCAATCTAAATATCTTATGATATATAAGATAATG 613  
DB |||||  
QY 650 TCCCTGCAACCCAGGAGATTAATTTGACCAATCTAATATTTATGATGATACATGACATA 709  
DB |||||  
QY 614 AAACGCTTGACTCAAAACACAGCCAAATTTGAAGTCTTACTTAACCAACCAAG 663  
DB |||||  
QY 710 AAATGTTGATTTCTAAAGATGTGAAGATTTGAAGTTTATCTTCTACGCAAAAG 759  
DB |||||

## RESULT 6

US-08-580-806-1  
; Sequence 1, Application US/08580806  
; Patent No. 5935568







```

; APPLICANT: Lee, John Scott
; APPLICANT: Pushko, Peter
; APPLICANT: Smith, Jonathan F.
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Vaccine Against Staphylococcus Intoxication
; FILE REFERENCE: Army-136
; CURRENT APPLICATION NUMBER: US/09/350,755A
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 97 (IBM compatible)
; SEQ ID NO 3
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-350-755A-3

Query Match      24.0%; Score 158.8; DB 4; Length 723;
Best Local Similarity 58.3%; Pred. No. 6.4e-28;
Matches 379; Conservative 0; Mismatches 226; Indels 45; Gaps 4;

QY      56  AAAATATATATTTTCTTTATCGAGGGTCACCCCTGTTACTCACGAGAAATGTGAAATCTCTGTG 115
DB      68  AARATATCAAGTTTTCGTATGATGATATATCATGTATCAGCAATTAACGTTAAATCTATAG 127

QY      116  ATCAACTTTTATCTCACATTAAATATATATATGTTTCAGGCCCCA-----AATTATG 166
DB      128  ATCAATTTTCGATACTTTTGACTTAAATATATCTATTAAGGACACTAAGTTAGGGAATTTATG 187

QY      167  ATAAATTTAAAAACCTGAACCTTAAGAACCAAGATGGCAACTTTATTTAAGGATAAAAACG 226
DB      188  ATAAATGTCGAGTCGAATTTTAAACCAAGAAATTTAGCTGATAATCAAGATAAATATACG 247

QY      227  TTGATATTTATGTTGTAGATATTACCATTCTCTCTATTTATGTGAAAA----- 275
DB      248  TAGATGTTGTTGAGCTAATGCTTTATTATCAATGCTGCTTTTCTTAAAAACGAATGATA 307

QY      276  -----TGCAGAAAGGAGTGATGTATCTACGGAGGGGTAAACAAATCATG 319
DB      308  TTAATTCGCATCAAACTGCACAAACGAAAAAAGCTTGTATGTTGGTGTAACTGAGCATA 367

QY      320  AAGGGATCATTTAGAAATTCCTTAAAGAGATGTCGTTAAAGTATCAATCGATGGTATCC 379
DB      368  ATGGAACCAATTAGATAAATATAGAAAGTATTACTGTTTCGGATTTTGAAGATGGTAAAA 427

QY      380  AAGACCTPATCATTTGATATTGAAACAAATAAAAAAATGGTAACCTGCCTCAAGAATTAGACT 439
DB      428  ATTATTATCTTTTGAGTCAAACTAATAAGAAAAAGGTGACUGCTCAAGAATTAGATT 487

QY      440  ATAAAGTTAGAAATATCTTACAGATAAATAGCAACTATATCTAATGGAACCTTCTAAAT 499
DB      488  ACCTAACTCGTCACTATTTCGGTAAAAAATAAAAAAAGCTCTATGAATTTAAACAACCTCGCCT 547

QY      500  ATGAAACCTGGATATAAAGCTTCATACCTTAAGATAAAGAAAGTTTTTGGTTTGAATTTTT 559
DB      548  ATGAAACGGATATATTAAATTTATA--GAAATGGAATAGCTTTTGTTGATGACATGA 604

QY      560  TCCTCGAACCAAG-----AATTTTACTCAATCTAAATATCTTATGATATAAAGATAATG 613
DB      605  TGCCTGCACAGGAGATAAATTTGACCAATCTAAATATTATTAATGATCTACAATGACATA 664

QY      614  AARCGCTTGACTCAACACAGGCAATTTGAAGTCTTACCTTAACAACCAAG 663
DB      665  AAATGGTTGATCTTAAAGATGTGAAGATTGAAGTTTATCTTACGACAAAG 714

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RESULT 10  
US-09-350-755A-2  
; Sequence 2, Application US/09350755A  
; Patent No. 6632640  
; GENERAL INFORMATION:  
; APPLICANT: United States Army Medical Research Institute of Infectious Diseases

```

; APPLICANT: Lee, John Scott
; APPLICANT: Pushko, Peter
; APPLICANT: Smith, Jonathan F.
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Vaccine Against Staphylococcus Intoxication
; FILE REFERENCE: Army-136
; CURRENT APPLICATION NUMBER: US/09/350,755A
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 97 (IBM compatible)
; SEQ ID NO 2
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-350-755A-2

Query Match      24.0%; Score 158.8; DB 4; Length 801;
Best Local Similarity 58.3%; Pred. No. 6.6e-28;
Matches 379; Conservative 0; Mismatches 226; Indels 45; Gaps 4;

Qy      56  AAAATATATATTTCTTTATGAGGGTCACCTGTTACTCACGAGAAATGTGAATCTCTGTG 115
Db      146  ABAATATGAAGTTTGTATGATGATGAATCATGTATCAGCAATTAACGTTAAATCTATAG 205

Qy      116  ATCAACTTTTATCTCACCAATTTAATAATATATATGTTTCAGGGCCA-----AATTATG 166
Db      206  ATCAATTTTCGATACTTTGACTTAAATATATCTATTAAAGGACACTAAGTTAGGGAATTTATG 265

Qy      167  ATAAATTA AAAACCTGAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGATTA AAAACG 226
Db      266  ATAAATGTCAGTCGAAATTTAAAAACAAGAAATTTAGCTGATTAATA CAAGAATAAAATACG 325

Qy      227  TTGATATTTATGGTGAGAAATATTACCATCTCTGTTATTTATGTGAAAA----- 275
Db      326  TAGATGTTTGAGCTAATGCTTTATATCAATGTGCTTTTCTTAA AAAACGAATGATGA 385

Qy      276  -----TGCAGAAAGGAGTGCATGTATCTACGAGGGGGTAACAAATCATG 319
Db      386  TTAATTCGCATCAAACTGACAAACGAAAACTTTGTATGTATGGTGTGTTAACTGAGCATA 445

Qy      320  AAGGGATCATTTAGAAATTCCTTAAAGAGATAGTCGTTAAAGTATCAATCGATGGTATCC 379
Db      446  ATGGAACCAATTAGATAAATATAGAAGTATTTACTGTTGGGGTATTTGAAGATGGTAAAA 505

Qy      380  AAAGCCTTATCATTTGTATTTGAAACAAATATAAAAAAATGTTAACTGCTCAAGAAATTAGACT 439
Db      506  ATTTATTATCTTTTGAGTACAACTAATAAGAAAAGGTGACTGCTCAAGAAATTAGATT 565

Qy      440  ATAAAGTTGAAAATATCTTACAGATPAATAAGCAACTATATATATAATGAGACCTTCTAAAT 499
Db      566  ACCTAACTCGTCTACTATTTGGTGA AAAAATAAAAAAACTCTATGAATTTAAACAACCTGCGCCT 625

Qy      500  ATCAAACTGGATATATAAGTTTCATACCTTAAGAAATAAGAAAGCTTTTTCGTTTGAATTTT 559
Db      626  ATGAACGGGATATATTAATTTTATA--GAAATGAGATAGCTTTTGTGTATGACATGA 682

Qy      560  TCCTTGAACCGAG-----AATTTACTCAATCTAAATATCTTATGATATATAAAGATAATG 613
Db      683  TGCCTGCACAGGAGATAAATTTTGACCAATCTAAATATTTTAATGATGTCACATGACATA 742

Qy      614  AAAGCCTTGACTCAAAACACAGCCAAATTTGAAGTCTTACCTTAACCAACG 663
Db      743  AAATGTTGATTTCTAAGATGTGAAGTGAAGTATTTATCTTACGACAAAG 792

```

RESULT 11  
US-09-144-776B-9  
; Sequence 9, Application US/09144776B  
; Patent No. 6399332  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Ulrich,

Mark A. Olson  
Sina Bavari  
TITLE OF INVENTION: Bacterial Superantigen  
Vaccines  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles H. Harris  
STREET: US Army MRC -504 Scott Street  
MCWR-JA (Charles H. Harris-Patent  
Atty)  
CITY: FORT DETRICK  
STATE: MARYLAND  
COUNTRY: USA  
ZIP: 21702-5012  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.5  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,776B  
FILING DATE: 01-Sep-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/882,431  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Charles H. Harris  
REGISTRATION NUMBER: 34,616  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 619-2065  
TELEFAX: (301) 619-7714  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1388  
TYPE: Nucleic Acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-144-776B-9

Query Match 24.0%; Score 158.8; DB 4; Length 1388;  
Best Local Similarity 58.3%; Pred. No. 7.4e-28;  
Matches 379; Conservative 0; Mismatches 226; Indels 45; Gaps 4;

QY 56 AAAATATATATTTCTTTATGAGGTGACCTGTTACTCAGGAGATGTGAATCTGTG 115  
DB 65 AAAATATGAAGTTTGTATGATGATAATCATGTATCAGCAATAAAGTTAAATCTATAG 124  
QY 116 ATCAACTTTTCTACCAATTAATATATATATATATATATATATATATATATATATAT 166  
DB 125 ATCAATTCGATCTTGTGCTTAATATATATATATATATATATATATATATATATATAT 184  
QY 167 ATAAATTAAGAACTGAACCTTAAGAACCAAGAGATGCACTTTATTAAGGATAAAGCG 226  
DB 185 ATAAATTCGATCGAATTTAAACAAAGATTTAGCTGATATATATATATATATATATAT 244  
QY 227 TTGATATTTATGTTGATGATATATATATATATATATATATATATATATATATATAT 275  
DB 245 TAGATGTTTGGAGCTAATGCTTATATATATATATATATATATATATATATATATATAT 304  
QY 276 -----TGCAAGAGAGTGCATGATCTACGAGGGGTAAACAAATCATG 319  
DB 305 TTAATTCGATCAAACTGCAACAAAGAAACCTGTATGATGTTGTTGTTGTTGTTGTTG 364  
QY 320 AAGGGAATCATTTAGAAATCTTAAAGAGATAGTCTGTTAAAGTATCAATCGATGTTATCC 379  
DB 365 ATGGAACCAATTTAGATAATATAGAGTATTTACCTGTCGGGTATTTGAGATGGTAA 424  
QY 380 AAGCCCTATCATTTGATTTGAAACAAATTAAGAAATGGTAACTGCTCAAGATTTAGACT 439

425 ATTATATATCTTTTGAAGTCAAACTAATAAGAAAAAGGTGACTGCTCAAGAAATTAGATT 484  
QY 440 ATAAAGTTAGAAATATCTTACAGATATATAGCAACTATATATATATATATATATATAT 499  
DB 485 ACCTAACTCGTCACTATTGTGAAATAAATAAATAAATAAATAAATAAATAAATAAATA 544  
QY 500 ATGAAACTGGAT 559  
DB 545 ATGAAACGGGAT 601  
QY 560 TCCCTGAACCGAG-----AATTTACTCAATCAATATATATATATATATATATATAT 613  
DB 602 TGCCTGCACCGAGAT 661  
QY 614 AAAGCCTTGACTCAACACAAAGCCAAATTTGAAGTCTACTTAACCAACCAAG 663  
DB 662 AAATGGTTGATTTAAAGATGTGAAGATGAAGTTTATCTTACGCAAG 711

RESULT 12  
US-09-144-776B-7  
; Sequence 7, Application US/09144776B  
; Patent No. 6399332  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Ulrich,  
; Mark A. Olson  
; Sina Bavari  
; TITLE OF INVENTION: Bacterial Superantigen  
; Vaccines  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles H. Harris  
; STREET: US Army MRC -504 Scott Street  
; MCWR-JA (Charles H. Harris-Patent  
; Atty)  
; CITY: FORT DETRICK  
; STATE: MARYLAND  
; COUNTRY: USA  
; ZIP: 21702-5012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.5  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/144,776B  
; FILING DATE: 01-Sep-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/882,431  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Charles H. Harris  
; REGISTRATION NUMBER: 34,616  
; REFERENCE/DOCKET NUMBER: <Unknown>  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 619-2065  
; TELEFAX: (301) 619-7714  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1712  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-144-776B-7

Query Match 24.0%; Score 158.8; DB 4; Length 1712;  
Best Local Similarity 58.3%; Pred. No. 7.8e-28;  
Matches 379; Conservative 0; Mismatches 226; Indels 45; Gaps 4;

QY 56 AAAATATATATTTCTTTATGAGGTGACCTGTTACTCAGGAGATGTGAATCTGTG 115



TOPOLOGY: Unknown  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-144-776B-3

Query Match 10.7%; Score 71; DB 4; Length 757;  
Best Local Similarity 47.8%; Pred. No. 1e-07;  
Matches 311; Conservative 0; Mismatches 325; Indels 15; Gaps 3;

QY 23 AACTTCACAGATCTAGTTAGTTAAACACCTTCAAAATATATATTTCTTTATGAGGTTG 82  
DB |||||  
QY 49 AATTGACGGAACAGCTTTAGGCAATCTTAAACAAATCTATTATTAACAATGAAAAGCTA 108  
DB |||||  
QY 83 ACCCTGTTTACTACAGATCTGGAATCTGTTGATCAACTTTTATCTCACCATTATATAT 142  
DB |||||  
QY 109 AAACCTGAAATATAGAGAGTCAAGTCAATTTTCGACAGATATATATTTTAAAGGCT 168  
DB |||||  
QY 143 ATAAATGTTTCAGGGCCAAATATATGATAATTAATAAAGTCAACTTAAAGAACCAAGAGATGG 202  
DB |||||  
QY 169 TTTTACAGATCAATTCGTTGATATACGATTTTATAGTACGTTTTCGATTCAAGGATATG 228  
DB |||||  
QY 203 CAACCTTTATTAAGGATATAAAGCTTGATATTTATGTTGTTAGATATTAACCTCTCTGTT 262  
DB |||||  
QY 229 TTGATAAATATTAAGGGAAGAAAGTAGACTTGATGTTGCTTATGCTGTTATCAATG-- 286  
DB |||||  
QY 263 ATTTATGTCGAAATGCAGAAAGGAGTGCATGTATCTACGGAGGGGTAAACAAATCATGAAG 322  
DB |||||  
QY 287 -TGCGGGTGGTACACCAACAAACAGCTTGATGTATGTTGTTGTTTACATGATA 345  
DB |||||  
QY 323 GGAATCATTTAGAAATTCCTTAAAGAGATGCTGTTAAAGTATCAATCGATGTTATCCAAA 382  
DB |||||  
QY 346 ATAAATCGATTGACCGAAGAAAGTGCAGATCAATTTATGGCTAGACGGTAAACAAA 405  
DB |||||  
QY 383 GCCTATCATTTGA-----TATTGAAACAAATATAAATAATGTTCTCAAGATTTAG 436  
DB |||||  
QY 406 ATACAGTACCTTTGGAAACGGTTTAAACCGAATTAAGAAATGTTAACTGTTCAAGAGTTGG 465  
DB |||||  
QY 437 ACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATATATCTATGACCTTCT- 495  
DB |||||  
QY 466 ATCTTCAAGCAAGACGTTATTTACAGGAAAATAATAATTTATATACTCTGATGTTTTG 525  
DB |||||  
QY 496 -----AAATATGAAACTGGATATATAAGTTTCATACCTAAGAAATAAGAAAGTTTTGTT 550  
DB |||||  
QY 526 ATGGGAAGGTTTCAGAGGGGATTAATCGTGTTCATCTTCTACAGAACCTTCGGTTAAT 585  
DB |||||  
QY 551 TTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATATCTTATGATATATAAGATA 610  
DB |||||  
QY 586 ACGATTTATTTGCTGCTCAAGGACAGTATTCAAATACACTATTAAAGAAATATATAGAGATA 645  
DB |||||  
QY 611 ATGAAACGCTTGACTCAAAACACAGCCAAATTTGAAGTCTACCTTAACCAACA 661  
DB |||||  
QY 646 ATAAACGATTAACTCTGAACATGCAATGATTTGATATATATATATATACAA 696  
DB |||||

## RESULT 15

US-09-350-755A-1  
Sequence 1, Application US/09350755A  
Patent No. 6632640  
GENERAL INFORMATION:  
APPLICANT: United States Army Medical Research Institute of Infectious Diseases  
APPLICANT: Lee, John Scott  
APPLICANT: Pushko, Peter  
APPLICANT: Smith, Jonathan F.  
APPLICANT: Ulrich, Robert G.  
TITLE OF INVENTION: Vaccine Against Staphylococcus Intoxication  
FILE REFERENCE: Army-136  
CURRENT APPLICATION NUMBER: US/09/350,755A  
CURRENT FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: US 60/092,416  
PRIOR FILING DATE: 1998-07-10  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Microsoft Word 97 (IBM compatible)  
SEQ ID NO 1

LENGTH: 757  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-09-350-755A-1

Query Match 10.7%; Score 71; DB 4; Length 757;  
Best Local Similarity 47.8%; Pred. No. 1e-07;  
Matches 311; Conservative 0; Mismatches 325; Indels 15; Gaps 3;

QY 23 AACTTCACAGATCTAGTTAGTTAAACACCTTCAAAATATATATTTCTTTATGAGGTTG 82  
DB |||||  
QY 49 AATTGACGGAACAGCTTTAGGCAATCTTAAACAAATCTATTATTAACAATGAAAAGCTA 108  
DB |||||  
QY 83 ACCCTGTTTACTACAGATCTGGAATCTGTTGATCAACTTTTATCTCACCATTATATAT 142  
DB |||||  
QY 109 AAACCTGAAATATAGAGAGTCAAGTCAATTTTCGACAGATATATATTTTAAAGGCT 168  
DB |||||  
QY 143 ATAAATGTTTCAGGGCCAAATATATGATAATTAATAAAGTCAACTTAAAGAACCAAGAGATGG 202  
DB |||||  
QY 169 TTTTACAGATCAATTCGTTGATATACGATTTTATAGTACGTTTTCGATTCAAGGATATG 228  
DB |||||  
QY 203 CAACCTTTATTAAGGATATAAAGCTTGATATTTATGTTGTTAGATATTAACCTCTCTGTT 262  
DB |||||  
QY 229 TTGATAAATATTAAGGGAAGAAAGTAGACTTGATGTTGCTTATGCTGTTATCAATG-- 286  
DB |||||  
QY 263 ATTTATGTCGAAATGCAGAAAGGAGTGCATGTATCTACGGAGGGGTAAACAAATCATGAAG 322  
DB |||||  
QY 287 -TGCGGGTGGTACACCAACAAACAGCTTGATGTATGTTGTTGTTTACATGATA 345  
DB |||||  
QY 323 GGAATCATTTAGAAATTCCTTAAAGAGATGCTGTTAAAGTATCAATCGATGTTATCCAAA 382  
DB |||||  
QY 346 ATAAATCGATTGACCGAAGAAAGTGCAGATCAATTTATGGCTAGACGGTAAACAAA 405  
DB |||||  
QY 383 GCCTATCATTTGA-----TATTGAAACAAATATAAATAATGTTCTCAAGATTTAG 436  
DB |||||  
QY 406 ATACAGTACCTTTGGAAACGGTTTAAACCGAATTAAGAAATGTTAACTGTTCAAGAGTTGG 465  
DB |||||  
QY 437 ACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATATATCTATGACCTTCT- 495  
DB |||||  
QY 466 ATCTTCAAGCAAGACGTTATTTACAGGAAAATAATAATTTATATACTCTGATGTTTTG 525  
DB |||||  
QY 496 -----AAATATGAAACTGGATATATAAGTTTCATACCTAAGAAATAAGAAAGTTTTGTT 550  
DB |||||  
QY 526 ATGGGAAGGTTTCAGAGGGGATTAATCGTGTTCATCTTCTACAGAACCTTCGGTTAAT 585  
DB |||||  
QY 551 TTGATTTTTCCTGAAACAGAAATTTACTCAATCTAAATATCTTATGATATATAAGATA 610  
DB |||||  
QY 586 ACGATTTATTTGCTGCTCAAGGACAGTATTCAAATACACTATTAAAGAAATATATAGAGATA 645  
DB |||||  
QY 611 ATGAAACGCTTGACTCAAAACACAGCCAAATTTGAAGTCTACCTTAACCAACA 661  
DB |||||  
QY 646 ATAAACGATTAACTCTGAACATGCAATGATTTGATATATATATATATATACAA 696  
DB |||||

Search completed: September 3, 2004, 18:58:10  
Job time : 82 secs

	Query Match	2.1%	Score 39.0001	DB 1	Length 1114
Best Local Similarity	46.8%	Fixed	No. 0.005		
Matches 123	Conservative	0	Mismatches 140	Indels	Gaps 0
597	ATATATAACATATTTTCATCTCTCCACCTACTATCTGCTAAAGATAAATAACTACTATTC				656
799	ATAAATCAGAAATATGTGATGCATCAAGCATCTCCTGTAATTTATTAATAAATAACTATTC				740
657	TTTTTTTTTGTTTTTATATAATAAATATTAATAATAGTTTAATGTTTTTTAAAAATATAC				716





Db	739	TTTTTTTTTACAAAAAATAAAATTTTTATTGGTTTTATAAICTATTAAAAATCAATATCT	680
Qy	717	AATTTATATCTATTATAGTTAGCTATTTTTTCATTGTTAGTAAATATTGGTGAATTTGTA	776
Db	679	TAGATGTTTTTTTTTATAAAGTAATCTTTTTTAAAGAAAGGTAAAGTTTTTACTATTACTGTTT	620
Qy	777	TAACTTTTTTAAATCTAGAGGAGAACCCAGATATAAAATGGAGGAATATTAAATGGAAAC	836
Db	619	TTCTTTTTATGAATAATTCCTGTAAACTGCAATCAAGTAATAGGGCTTTGTAAACA	560
Qy	837	AATAAAAAGTATTGAAGAAAT	859
Db	559	TCAAAATTATTGTATGGAGAAAT	537

## RESULT 2

US-08-304-732B-25  
Sequence 25, Application US/08304732B  
GENERAL INFORMATION:  
APPLICANT: BERGERON, Michel G.  
APPLICANT: CUELLETTE, Marc  
APPLICANT: ROY, Paul H.  
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY  
TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY  
TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY  
NUMBER OF INVENTION: LABORATORY  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 411 East Wisconsin Avenue  
CITY: Milwaukee  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53202-4497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,732B  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BAKER, Jean C.  
REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 850586.90012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5000  
TELEFAX: (414) 277-5591  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1114 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Haemophilus influenzae  
US-08-304-732B-25

### RESULT 3

US-08-304-732B-35/c

Sequence 35, Application US/08304732B

GENERAL INFORMATION:

APPLICANT: BERGERON, Michel G.

APPLICANT: OUELLETTE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY

TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY

TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY

TITLE OF INVENTION: LABORATORY

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles & Brady

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: USA

ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/304,732B

FILING DATE: 12-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 850586.90012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 277-5000

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 5953 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Lactococcus lactis

US-08-304-732B-35

Query Match

Best Local Similarity 50.3%; Score 30; DB 1; Length 5953;

Matches 97; Conservative 0; Mismatches 90; Indels 6; Gaps 1;

QY 609 TTTTCATCTCTCACTATCTATCTGTAAGAGATAAAATAACTATGTTTTTTTGTGA 668

DB 257 TTTTTCATGCCACCACTAGCTTGGTAAATATAAAAAATAGCTTTTAACTTGCTT 198

QY 669 TTTTATAATAAAATTAATAATAAGTTAAATGTTTTTAAAAAATATACAAATTTATCTA 728

DB 197 TTTTCT-----TTTTTAATAAGATAAGGTCCTATTATTTAGTCTCTTACCTTATGAG 144

QY 729 TTTATAGTTAGCTAATTTTTTCATTTGTTAGTAAATATGCTGAATGCTAATACCTTTTAA 788

DB 143 AATAAAATCTTTGATTTTTTACGTAGAAATGNTTTTTTAACTTAATTTTATT 84

QY 789 ATCTAGAGAGGAA 801

DB 83 AATAATAGTAGA 71

RESULT 4

US-08-304-732B-31

Sequence 31, Application US/08304732B

GENERAL INFORMATION:

APPLICANT: BERGERON, Michel G.







APPLICATION NUMBER: US/08/304,732B  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BAKER, Jean C.  
REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 850586.90012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5000  
TELEFAX: (414) 277-5591  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 258 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Staphylococcus saprophyticus  
US-08-304-732B-24

Query Match 1.5%; Score 27.5; DB 1; Length 258;  
Best Local Similarity 48.0%; Pred. No. 0.92;  
Matches 106; Conservative 0; Mismatches 110; Indels 5; Gaps 1;  
QY 515 AAATATCTTCCTGTTTACGCTATCGCTACTGTCACCTAAATATACCCCTTATC 574  
DB 10 AATTACATTCGCTCATACGACGACGACGACGACGACGACGACGACGACGAC 69  
QY 575 AATGCTCTCTTAACCTCATCATATATACATATTC-----ATCCCTCTACCTACTA 629  
DB 70 TTGACTCTTAACATCTGTCTAAATTTGTTTATCTTCTGCTGCTAGAAATTTA 129  
QY 630 TCGTAAAGATAAATACATATGTTTGTGTTTATTTATTAATAAATATTAAT 689  
DB 130 CTCTAATCTCTGTTATTCATATTCATATTCATATTAATAATCATATGATCATTG 189  
QY 690 ATAAGTTAATGTTTAAAAATATACATTTTATCTATT 730  
DB 190 ATGAATCTGTTATCTGACATACAGGAGTGTCTCATT 230

## RESULT 7

US-08-304-732B-27  
Sequence 27, Application US/08304732B  
GENERAL INFORMATION:  
APPLICANT: BERGERON, Michel G.  
APPLICANT: OUELLETTE, Marc  
APPLICANT: ROY, Paul H.  
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY  
DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY  
OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY  
LABORATORY  
TITLE OF INVENTION: LABORATORY  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 411 East Wisconsin Avenue  
CITY: Milwaukee  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53202-4497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,732B  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BAKER, Jean C.  
REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 850586.90012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5000  
TELEFAX: (414) 277-5591  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9100 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Haemophilus influenzae  
US-08-304-732B-27

Query Match 1.5%; Score 27; DB 1; Length 9100;  
Best Local Similarity 51.2%; Pred. No. 1.4;  
Matches 63; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 668 ATTTTATAAAATTTATTAATAAGTTAATGTTTAAAAAATATACATTTTCT 727  
DB 5981 ATTAAGTTTAAAGGAGATTATGAAGATATTTTAAAGTGGGTTATTTTAGT 6040  
QY 728 ATTTAGTTAGCTATTTTTCATGTTAGTAAATTTGGTGAATTTGTAATACCTTTTA 787  
DB 6041 AGTTTGTGTCCTAATGCTTTTGTCTAATCTCTAAACAGATAACGAACTTTT 6100  
QY 788 AAT 790  
DB 6101 TAT 6103

## RESULT 8

US-08-304-732B-1  
Sequence 1, Application US/08304732B  
GENERAL INFORMATION:  
APPLICANT: BERGERON, Michel G.  
APPLICANT: OUELLETTE, Marc  
APPLICANT: ROY, Paul H.  
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY  
DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY  
OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY  
LABORATORY  
TITLE OF INVENTION: LABORATORY  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 411 East Wisconsin Avenue  
CITY: Milwaukee  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53202-4497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,732B  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BAKER, Jean C.  
REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 850586.90012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5000  
TELEFAX: (414) 277-5591  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1817 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear



MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE: Enterococcus faecalis  
 ORGANISM: Enterococcus faecalis  
 US-08-304-732B-1

Query Match 1.4%; Score 26.4; DB 1; Length 1817;  
 Best Local Similarity 51.7%; Pred. No. 1.7;  
 Matches 60; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
 QY 1306 CATTTCATTTGAACAAATAAATAATGGTAAGTCTCAAGAAATTAGACTATAAGTTA 1365  
 DB 618 CAATCGTGAAGAGGAGTAAATAATTTGTTCTCTGATATCCAGAACTTAAGATC 677  
 QY 1366 GAAAATATCTTACAGATATAGCAACTATATATATATGACCTTCTTAATATGAA 1421  
 DB 678 TTGCTTTTAGTATTGCAACGTTAAATAATGAGGCAATTAATTTTATAA 733

## RESULT 9

US-08-304-732B-15  
 Sequence 15, Application US/08304732B  
 GENERAL INFORMATION:  
 APPLICANT: BERGERON, Michel G.  
 APPLICANT: OUELLETTE, Marc  
 APPLICANT: ROY, Paul H.  
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY  
 TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY  
 TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY  
 TITLE OF INVENTION: LABORATORY  
 NUMBER OF SEQUENCES: 134  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Quarles & Brady  
 STREET: 411 East Wisconsin Avenue  
 CITY: Milwaukee  
 STATE: Wisconsin  
 COUNTRY: USA  
 ZIP: 53202-4497  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/304,732B  
 FILING DATE: 12-SEP-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BAKER, Jean C.  
 REGISTRATION NUMBER: 35,433  
 REFERENCE/DOCKET NUMBER: 850586.90012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (414) 277-5591  
 TELEFAX: (414) 277-5000  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1348 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: Proteus mirabilis  
 US-08-304-732B-15

Query Match 1.4%; Score 25.4; DB 1; Length 1348;  
 Best Local Similarity 48.9%; Pred. No. 2.7;  
 Matches 68; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
 QY 1304 ATCATTTCATTTGAACAAATAAATAATGGTAAGTCTCAAGAAATTAGACTATAAGT 1363  
 DB 13 ATCAATCTTAAAGAAATTAATAATTAATTAAGTGAATGATGATATACAGTAAAT 72  
 QY 1364 TAGAATAATCTTACAGATAAAGCAACTATATATACTAAATGGACCTTCTTAATATGAAC 1423

Db 73 GAGTTTCAACAGCAAAATCATATAGCTTTTAATGTTAGTACCCATCTTTATGCTTAC 132  
 QY 1424 TGGATATATAAAGTTTCATA 1442  
 Db 133 TGCCCGAGAGGAGATAACA 151

## RESULT 10

US-08-304-732B-27/c  
 Sequence 27, Application US/08304732B  
 GENERAL INFORMATION:  
 APPLICANT: BERGERON, Michel G.  
 APPLICANT: OUELLETTE, Marc  
 APPLICANT: ROY, Paul H.  
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY  
 TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY  
 TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY  
 TITLE OF INVENTION: LABORATORY  
 NUMBER OF SEQUENCES: 134  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Quarles & Brady  
 STREET: 411 East Wisconsin Avenue  
 CITY: Milwaukee  
 STATE: Wisconsin  
 COUNTRY: USA  
 ZIP: 53202-4497  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/304,732B  
 FILING DATE: 12-SEP-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BAKER, Jean C.  
 REGISTRATION NUMBER: 35,433  
 REFERENCE/DOCKET NUMBER: 850586.90012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (414) 277-5000  
 TELEFAX: (414) 277-5591  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9100 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: Haemophilus influenzae  
 US-08-304-732B-27

Query Match 1.4%; Score 25.4; DB 1; Length 9100;  
 Best Local Similarity 49.6%; Pred. No. 2.8;  
 Matches 65; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
 QY 560 AATATACCCCTTATCAATCGCTTCTTAAACCTCATCTATATATACATATTTTCATCTCC 619  
 Db 8079 AATAATACGCTTATCGGCTTTTTCAGTCTTATATTAAGTCTGTCGCCAGCCCC 8020  
 QY 620 TACTATCTATTCGTAAGAAGATAAATAACTATGTTTTTTTGTGTTATTTTATAATA 679  
 Db 8019 ACATCTGAATCTCTCCACACCTAATTTTCGCAACAATTTTGAGATTTTCATTGAGT 7960  
 QY 660 AATTATTATA 690  
 Db 7959 AACCAAGTAGTA 7949

## RESULT 11

US-08-304-732B-26









REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 850586.90012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5000  
TELEFAX: (414) 277-5591  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2275 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE: faecalis  
ORGANISM: Enterococcus faecalis

US-08-304-732B-2

Query Match 1.3%; Score 23.2; DB 1; Length 2275;  
Best Local Similarity 46.8%; Pred. No. 7.3;  
Matches 73; Conservative 0; Mismatches 83; Indels 0; Gaps 0;  
QY 450 TCTTCCACTCTCTACCGTCAACTTCATCATCTCTCACTTTTTCGTGTGTACACA 509  
DB 1339 TCTTTATGTTTGTATGACATCCGATCCGATCCGATCCGATCCGATCCGATCCGAT 1280  
QY 510 TAATCAATATCTTCGTTTACGACTATCGTACTGTGTCACCTAAATATACCCC 569  
DB 1279 TGTTCAGTAAGTCGGTGTTCCTTCAATATATGCGCACTTCTTCTGCTAAAGGTGAA 1220  
QY 570 TTATCAATCGCTTCCTTAAACTCATCTATATATAC 605  
DB 1219 CCACCAATCATATTTTTCACAGCGATATATCCAGC 1184

#### RESULT 14

US-08-304-732B-1/c  
Sequence 1, Application US/08304732B  
GENERAL INFORMATION:  
APPLICANT: BERGERON, Michel G.  
APPLICANT: OUELLETTE, Marc  
APPLICANT: ROY, Paul H.  
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY  
TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY  
TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY  
TITLE OF INVENTION: LABORATORY  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESS: 134  
ADDRESS: Quares & Brady  
STREET: 411 East Wisconsin Avenue  
CITY: Milwaukee  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53202-4497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,732B  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BAKER, Jean C.  
REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 850586.90012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5000  
TELEFAX: (414) 277-5591  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1817 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE: faecalis  
ORGANISM: Enterococcus faecalis  
US-08-304-732B-1  
Query Match 1.2%; Score 22.6; DB 1; Length 1817;  
Best Local Similarity 45.7%; Pred. No. 9.5;  
Matches 79; Conservative 0; Mismatches 94; Indels 0; Gaps 0;  
QY 1009 CTCAGAGAAATGCAATCTGTTGATCACTTTATCTCACCATTATATATATGTTT 1068  
DB 1102 CCTCGATCATACTGTTGTTGGAATGATCTTCATATATGTTTCACAAATTT 1043  
QY 1069 CAGGCGCAATATGATAAATTAAGAACTGAACCTTAAGAACCAAGAGATGCGAACTTTAT 1128  
DB 1042 TCCATGCGTATAGCGGTCAATAGCAATTCGATTAATGTCGTAGTGGCGCTTGAAT 983  
QY 1129 TTAAGGATAAAGCGTTGATATTTATGTTGATAGAAATATTACCATCTCTGTTAT 1181  
DB 982 ATAGATAAATATTTTGGCATCACTACTGTCATGCTAAACCCCTGTTAT 930

#### RESULT 15

US-08-304-732B-26/c  
Sequence 26, Application US/08304732B  
GENERAL INFORMATION:  
APPLICANT: BERGERON, Michel G.  
APPLICANT: OUELLETTE, Marc  
APPLICANT: ROY, Paul H.  
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY  
TITLE OF INVENTION: DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY  
TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY  
TITLE OF INVENTION: LABORATORY  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESS: 134  
ADDRESS: Quares & Brady  
STREET: 411 East Wisconsin Avenue  
CITY: Milwaukee  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53202-4497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,732B  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BAKER, Jean C.  
REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 850586.90012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5000  
TELEFAX: (414) 277-5591  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1598 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE: faecalis  
ORGANISM: Haemophilus influenzae  
US-08-304-732B-26

Query Match 1.2%; Score 22.4; DB 1; Length 1598;  
Best Local Similarity 52.1%; Pred. No. 10;  
Matches 50; Conservative 0; Mismatches 46; Indels 0; Gaps 0;



Qy	562	TATACCCCTTATCAATCGCTTCTTTAAACTCATCTATATATACATATTTCATCCTCCTA	621
Db	371	TATTCCTTTTCATCCCAATCTGATTTGTTATTATCTGAGCATAGAAGTTACATCACCATT	312
Qy	622	CCTATCTATTTCGTAATAAAGATAAAATAACTATTGT	657
Db	311	CATATTAAATTTCTAGAAATCAATATATAACGCCACCTGT	276

Search completed: May 11, 2004, 16:57:10  
Job time : 60 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 17:12:26 ; Search time 373 Seconds  
(without alignments)  
7551.087 Million cell updates/sec

Title: US-10-625-221-12\_COPY\_918\_1580  
Perfect score: 663  
Sequence: 1 caacaagaccgcgtacaaag.....aagctacctaacaacccaag 663

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N Geneseq 29Jan04.\*  
1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002s.\*  
7: geneseqn2003as.\*  
8: geneseqn2003bs.\*  
9: geneseqn2003cs.\*  
10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	100.0	1851	2	AAT51716
2	663	100.0	1851	2	AAV41593
3	661.4	99.8	756	4	AAH01002
4	661.4	99.8	1837	2	AAT28540
5	661.4	99.8	1837	4	ABA76857
6	658.2	99.3	1837	3	AAZ51112
7	658.2	99.3	1837	6	ABN84229
8	658.2	99.3	1837	7	ACA61184
9	658.2	99.3	1837	8	AAD56771
10	656.6	99.0	1837	8	ACD28901
11	651.8	98.3	1419	8	ACD28908
12	651.8	98.3	1419	8	AAD56778
13	582.6	87.9	1031	7	ACA64700
14	167.4	25.2	1095	7	ACA64696
15	166.8	25.2	773	2	AAT45698
16	166.8	25.2	801	7	ACA64688
17	166.8	25.2	886	7	ACA64689
18	166.8	25.2	1712	3	AAZ51107
19	166.8	25.2	1712	6	ABN84224
20	166.8	25.2	1712	7	ACA61179
21	166.8	25.2	1712	7	ACA64695
22	166.8	25.2	1712	8	ACD28896
23	166.8	25.2	1712	8	AAD56766

24	164.2	24.8	1095	3	AAZ51111
25	164.2	24.8	1095	6	ABN84228
26	164.2	24.8	1095	7	ACA61183
27	164.2	24.8	1095	8	ACD28900
28	164.2	24.8	1095	8	AAZ56770
29	159.2	24.0	867	4	AAH74983
30	158.8	24.0	723	3	AAZ45835
31	158.8	24.0	801	3	AAZ45834
32	158.8	24.0	1388	3	AAZ51109
33	158.8	24.0	1388	6	ABN84226
34	158.8	24.0	1388	7	ACA61181
35	158.8	24.0	1388	8	ACD28898
36	158.8	24.0	1388	8	AAZ56768
37	158.8	24.0	1712	3	AAZ51108
38	158.8	24.0	1712	6	ABN84225
39	158.8	24.0	1712	7	ACA61180
40	158.8	24.0	1712	8	ACD28897
41	158.8	24.0	1712	8	AAZ56767
42	112	16.9	815	3	AAA09240
43	96.6	14.6	1136	7	ACA64697
44	79	11.9	1443	7	ACA64694
45	77.4	11.7	774	9	ADD44369

## ALIGNMENTS

RESULT 1  
AAT51716  
ID AAT51716 standard; DNA; 1851 BP.  
XX  
AC AAT51716;  
XX  
DT 04-NOV-1997 (first entry)  
XX  
DE Streptococcus pyogenes Streptococcal toxin A DNA.  
XX  
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;  
KW protection; treatment; cancer; neutralising antibody;  
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;  
KW hypotension; group A streptococcal infection; myositis; fasciitis;  
KW liver damage; T cell; lymphoma; ovarian; uterine; ss.  
XX  
OS Streptococcus pyogenes.  
XX  
Key Location/Qualifiers  
CDS 828..1583  
FT /\*tag= a  
FT sig\_peptide 828..917  
FT /\*tag= b  
FT mat\_peptide 918..1580  
FT /\*tag= c  
FT /product= "Streptococcal\_toxin\_A"  
XX  
WO9640930-A1.  
XX  
PD 19-DEC-1996.  
XX  
XX 07-JUN-1996; 96WO-US010252.  
XX  
XX 07-JUN-1995; 95US-00480261.  
XX (MINU) UNIV MINNESOTA.  
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;  
XX WPI; 1997-099936/09.  
XX P-PSDB; AAW12097.  
XX Mutant SPE-A toxin with at least one amino acid change is substantially  
XX non-lethal - used in vaccine composition for treatment of cancer and  
XX streptococcal toxic shock syndrome etc.

PS Disclosure; Page 77-79; 102pp; English.

XX The present sequence encodes Streptococcus pyogenes Streptococcal toxin A (SPE-A), from which a non-lethal mutant SPE-A, comprising at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fasciitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells

XX Sequence 1851 BP; 635 A; 326 C; 248 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 663; DB 2; Length 1851;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGAACTTCAAAAT 60  
Db |||||  
QY 918 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGAACTTCAAAAT 977  
Db |||||

QY 61 ATATATTTCTTTATGAGGGTGACCTGTTACTCAGAGAATGTGAATCTGTGATCAA 120  
Db |||||

QY 978 ATATATTTCTTTATGAGGGTGACCTGTTACTCAGAGAATGTGAATCTGTGATCAA 1037  
Db |||||

QY 121 CTTTATCTCACCATTAAATATATATATGTTTCAGGGCCAAATATGATAAATAAAAACT 180  
Db |||||

QY 1038 CTTTATCTCACCATTAAATATATATGTTTCAGGGCCAAATATGATAAATAAAAACT 1097  
Db |||||

QY 181 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAGGATAAAAACTGTTGATATGTT 240  
Db |||||

QY 1098 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATAAAAACTGTTGATATGTT 1157  
Db |||||

QY 241 GTAGATATTTACCATCTCTGTTATTTATGTAAGAAATGCAGAGAGTGATCTATCTAC 300  
Db |||||

QY 1158 GTAGATATTTACCATCTCTGTTATTTATGTAAGAAATGCAGAGAGTGATCTATCTAC 1217  
Db |||||

QY 301 GGAGGGGTAAACAATCATGAAGGGAATCATTTAGAAATTCCTAAAAGATAGTCGTTAAA 360  
Db |||||

QY 1218 GGAGGGGTAAACAATCATGAAGGGAATCATTTAGAAATTCCTAAAAGATAGTCGTTAAA 1277  
Db |||||

QY 361 GTATCAATCGATGGTATCCAAAGCCATCATTTGATGAAACAAATAAAAAATGGTA 420  
Db |||||

QY 1278 GTATCAATCGATGGTATCCAAAGCCATCATTTGATGAAACAAATAAAAAATGGTA 1337  
Db |||||

QY 421 ACTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATAATGAACACTATAT 480  
Db |||||

QY 1338 ACTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATAATGAACACTATAT 1397  
Db |||||

QY 481 ACTATGGACCTTTAAATATGAACCTGGATATATAAGTTTCATACCTAAGATAAAGAA 540  
Db |||||

QY 1398 ACTAATGGACCTTTAAATATGAACCTGGATATATAAGTTTCATACCTAAGATAAAGAA 1457  
Db |||||

QY 541 AGTTTTTGGTTGATTTTTTCCCTGAACAGAAATTTACTCAATCTAAATATCTTATGATA 600  
Db |||||

QY 1458 AGTTTTTGGTTGATTTTTTCCCTGAACAGAAATTTACTCAATCTAAATATCTTATGATA 1517  
Db |||||

QY 601 TATAAGATAATGAACCGTTGACTCAACACAGAGCCAAATTTGAAGTCTACCTAACAACC 660  
Db |||||

QY 1518 TATAAGATAATGAACCGTTGACTCAACACAGAGCCAAATTTGAAGTCTACCTAACAACC 1577  
Db |||||

QY 661 AAG 663  
Db |||||

QY 1578 AAG 1580

RESULT 2

AAV411593

ID AAV411593 standard; DNA; 1851 BP.

XX AAV41593;

XX 12-OCT-1998 (first entry)

XX Nucleotide sequence of Streptococcus pyogenes exotoxin A.

XX SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;  
XX wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;  
XX streptococcal toxic shock syndrome; STSS; T cell lymphoma;  
XX uterine cancer; ss.

XX Streptococcus pyogenes.

XX Key Location/Qualifiers  
XX CDS 828..1583  
XX /\*tag= a

XX /product= "SPE-A toxin"

XX WO9824911-A2.

XX 11-JUN-1998.

XX 05-DEC-1997; 97WO-US022228.

XX 06-DEC-1996; 96US-0032930P.

XX (MINU) UNIV MINNESOTA.

XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

XX WPI; 1998-333330/29.

XX P-PSDB; AAW59780.

XX New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or  
XX treatment of streptococcal infection or toxic shock syndrome.

XX Disclosure; Fig 3; 95pp; English.

XX This is the nucleotide sequence of the Streptococcus pyogenes exotoxin A  
XX (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least 1  
XX aa change and is nonlethal compared with a protein to wild type SPE-A  
XX toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies  
XX that neutralise wild type SPE-A toxin activity. The toxins can be used in  
XX vaccines and therapeutics to generate a protective immune response  
XX against streptococcal infection. They can be used to protect against the  
XX development of streptococcal toxic shock syndrome (STSS). In addition,  
XX the toxins can be used for treating animals with symptoms of  
XX streptococcal infection or STSS and in methods for stimulating T cell  
XX proliferation and in the treatment of cancer. In particular they can be  
XX used for treating T cell lymphomas, and ovarian and uterine cancer

XX Sequence 1851 BP; 635 A; 326 C; 248 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 663; DB 2; Length 1851;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGAACTTCAAAAT 60

Db 918 CAACAAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTAAAGAACTTCAAAAT 977

QY 61 ATATATTTCTTTATGAGGGTGACCTGTTACTCAGAGAATGTGAATCTGTGATCAA 120

Db 978 ATATATTTCTTTATGAGGGTGACCTGTTACTCAGAGAATGTGAATCTGTGATCAA 1037

QY 121 CTTTATCTCACCATTAAATATATATGTTTCAGGGCCAAATATGATAAATAAAAACT 180

Db 1038 CTTTATCTCACCATTAAATATATGTTTCAGGGCCAAATATGATAAATAAAAACT 1097

QY 181 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATAAAAACTGTTGATATGTT 240

Db 1098 GAACCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATAAAAACTGTTGATATGTT 1157



QY 241 GTAGAAATATACCATCTCTGTTATTTATCTGAATGCGAAGGAGTCCATGTATCTAC 300  
 Dd |||||  
 QY 1158 GTAGAAATATACCATCTCTGTTATTTATGTGAAATGCGAAGGAGTCCATGTATCTAC 1217  
 Dd |||||  
 QY 301 GGAGGGGTAAACAAATCATCAAGGGGAATCATTTAGAAATTCCTTAAAGAGTAGTCGTTAAA 360  
 Dd |||||  
 QY 1218 GGAGGGGTAAACAAATCATCAAGGGGAATCATTTAGAAATTCCTTAAAGAGTAGTCGTTAAA 1277  
 Dd |||||  
 QY 361 GTATCAATCGATGGTATCAAGGCTATCATTTGATTTGAAACAAATTAAGAAATGTA 420  
 Dd |||||  
 QY 1278 GTATCAATCGATGGTATCAAGGCTATCATTTGATTTGAAACAAATTAAGAAATGTA 1337  
 Dd |||||  
 QY 421 ACTGCTCAAGAAATAGATATATAAGTTAGAAAATCTTACAGATAAAGCAACTATAT 480  
 Dd |||||  
 QY 1338 ACTGCTCAAGAAATAGATATATAAGTTAGAAAATCTTACAGATAAAGCAACTATAT 1397  
 Dd |||||  
 QY 481 ACTAATGACCTTCTTAATATGAACACTGGATATATAAAGTTTCAATACCTAAGAAATAAGAA 540  
 Dd |||||  
 QY 1398 ACTAATGACCTTCTTAATATGAACACTGGATATATAAAGTTTCAATACCTAAGAAATAAGAA 1457  
 Dd |||||  
 QY 541 AGTTTGTGTTGATTTTCCCTGACCAACAGAAATTTACTCAATCTAAATATCTTATGATA 600  
 Dd |||||  
 QY 1458 AGTTTGTGTTGATTTTCCCTGACCAACAGAAATTTACTCAATCTAAATATCTTATGATA 1517  
 Dd |||||  
 QY 601 TATAAGATAATGAACGCTTGACTCAACCAACAGCAAAATTTGAAGTCTACCTAACRACC 660  
 Dd |||||  
 QY 1518 TATAAGATAATGAACGCTTGACTCAACCAACAGCAAAATTTGAAGTCTACCTAACRACC 1577  
 Dd |||||  
 QY 661 AAG 663  
 Dd |||||  
 QY 1578 AAG 1580

## RESULT 3

AAH01002 ID AAH01002 standard; DNA; 756 BP.  
 XX AC AAH01002;  
 XX DT 24-JUL-2001 (first entry)  
 XX DE Unidentified nucleotide sequence SEQ ID NO:993.

XX Species specific; genus specific; family specific; probe; detection;  
 XX identification; algal; archaeal; bacterial; fungal; parasitological;  
 XX microorganism; diagnosis; translation elongation factor Tu; toxin;  
 XX translation elongation factor G; RecA recombinase; resistance;  
 XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;  
 XX primer; ds.

## Unidentified.

XX WO200123604-A2.  
 XX PD 05-APR-2001.  
 XX PF 28-SEP-2000; 2000WO-CA001150.  
 XX PR 28-SEP-1999; 99CA-02283458.  
 XX PR 19-MAY-2000; 2000CA-02307010.

XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX PA Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;  
 XX PI Picard FJ, Roy PH;  
 XX DR WPI; 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers  
 XX which can be used to identify and detect the presence of algal, archaeal,  
 XX bacterial, fungal and parasitological species in a test sample.

PS Disclosure; Page 957; 1580pp; English.

XX The present invention describes a method for generating a repository of  
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes  
 CC and/or primers are derived. The method comprises amplifying the nucleic  
 CC acids of determined algal, archaeal, bacterial, fungal and parasitological  
 CC species with a combination of defined primer pairs. The method can be  
 CC used for producing probes and/or primers for detecting one or more  
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and  
 CC parasites, for universal detection and for specific and ubiquitous  
 CC detection and identification of an algal, archaeal, bacterial, fungal and  
 CC parasitological species, genus, family and group. A nucleic acid (I) obtained  
 CC using the method of the invention can be used for the universal detection  
 CC of any bacterium, fungus or parasite in a sample and for the detection of  
 CC at least one antimicrobial agent resistance gene or at least one toxin  
 CC gene. hexA nucleic acids are used for the specific and ubiquitous  
 CC detection and for identification of Streptococcus pneumoniae. (I) can be  
 CC used to design a therapeutic agent which is effective against  
 CC microorganisms. Microbial species or genus or family or phylum or group  
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,  
 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,  
 CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria  
 CC gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster  
 CC results than substrate specificity tests as results can be determined in  
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002104  
 CC represent nucleotide sequences and primers/probes which are given in the  
 CC exemplification of the present invention

Sequence 756 BP; 297 A; 110 C; 118 G; 231 T; 0 U; 0 Other;

Query Match 99.8%; Score 561.4; DB 4; Length 756;

Best Local Similarity 99.8%; Pred. No. 2e-120;

Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 60  
 Dd |||||  
 QY 91 CAACAAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 150  
 Dd |||||  
 QY 61 ATATATTTCTTTATGAGGGTGACCCGTGTTACTCACGAGAAATGTGAATCTGTTGATCAA 120  
 Dd |||||  
 QY 151 ATATATTTCTTTATGAGGGTGACCCGTGTTACTCACGAGAAATGTGAATCTGTTGATCAA 210  
 Dd |||||  
 QY 121 CTGTTATCTCACCATTTAATATATATGTTTCAGGGCCAAATATGATAAATTAATAA 180  
 Dd |||||  
 QY 211 CTGTTATCTCACCATTTAATATATGTTTCAGGGCCAAATATGATAAATTAATAA 270  
 Dd |||||  
 QY 181 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATTAAGCACTGTTATTTATGTT 240  
 Dd |||||  
 QY 271 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATTAAGCACTGTTATTTATGTT 330  
 Dd |||||  
 QY 241 GTAGAATATTACCATCTCTGTTATTTATGTAATGCAAGAGGAGTGCATGTATCTAC 300  
 Dd |||||  
 QY 331 GTAGAATATTACCATCTCTGTTATTTATGTAATGCAAGAGGAGTGCATGTATCTAC 390  
 Dd |||||  
 QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCAATTTAGAAATTCCTTAAAGAGTAGTCGTTAAA 360  
 Dd |||||  
 QY 391 GGAGGGGTAAACAAATCATGAAGGGAATCAATTTAGAAATTCCTTAAAGAGTAGTCGTTAAA 450  
 Dd |||||  
 QY 361 GTATCAATCGATGGTATCCAAAGCCCTATCATTTGATATTGAAACAAATTAAGAAATGCGTA 420  
 Dd |||||  
 QY 451 GTATCAATCGATGGTATCCAAAGCCCTATCATTTGATATTGAAACAAATTAAGAAATGCGTA 510  
 Dd |||||  
 QY 421 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATATCTTACAGATAAAGCAACTATAT 480  
 Dd |||||  
 QY 511 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATATCTTACAGATAAAGCAACTATAT 570  
 Dd |||||  
 QY 481 ACTAATGAGCACTTCTTAATATGAACCTGGATATATAAAGTTCTATACCTAAGAAATAAGAA 540  
 Dd |||||  
 QY 571 ACTAATGAGCACTTCTTAATATGAACCTGGATATATAAAGTTCTATACCTAAGAAATAAGAA 630  
 Dd |||||  
 QY 541 AGTTTGTGTTGATTTTCCCTGACCAACAGAAATTTACTCAATCTAAATATCTTATGATA 600  
 Dd |||||  
 QY 631 AGTTTGTGTTGATTTTCCCTGACCAACAGAAATTTACTCAATCTAAATATCTTATGATA 690  
 Dd |||||



XX 29-JUN-2001.  
 PD 12-SEP-1995; 95NZ-00501596.  
 XX 12-SEP-1995; 95NZ-00501596.  
 PF 12-SEP-1995; 95NZ-00501596.  
 XX (IDII-) IDI INFECTIO DIAGNOSTIC INC.  
 XX Bergeron MG, Ouellette M, Roy PH;  
 PI WPI; 2001-615034/71.  
 XX  
 XX Method for detecting target bacterial species in a sample, comprises  
 PT detecting the presence or amount of bacterial nucleic acid amplified by a  
 PT primer derived from bacterial DNA, specific for the target bacterial  
 PT species.  
 XX  
 PS Claim 6; Page 107-108; 168pp; English.  
 XX  
 CC The invention relates to detecting target bacterial species suspected to  
 CC be present in a sample, comprising contacting nucleic acids of target  
 CC bacterial species with an amplification primer pair derived from a  
 CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target  
 CC bacterial species but ubiquitous for different strains, amplifying the  
 CC nucleic acid and detecting the presence or amount of an amplified  
 CC sequence as an indication of the presence or amount of the target  
 CC bacterial species. The invention includes primers and probes (ABA76862-  
 CC ABA76984) against the target bacterial species, especially E.coli,  
 CC K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae, S.aureus,  
 CC S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes, H.influenzae,  
 CC M.catarrhalis and/or group A Streptococci producing exotoxin A gene spe  
 CC A, suspected to be present in a sample which is obtained from human  
 CC patients, animals, environment or food, and which consists of one or more  
 CC bacterial colonies. Oligonucleotide probes and primers complementary to  
 CC the bacterial genes encoding resistance to antibiotics such as bla(tem),  
 CC bla(tob), bla(shv), aadB, aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH,  
 CC vanX, satA, aacA-phd, vat, yga, msrA, sul and/or int (ABA76985-ABA77001)  
 CC are also useful to identify commonly encountered and clinically important  
 CC resistance genes. The invention provides a rapid method of bacterial  
 CC identification that can be achieved, which reduces the time currently  
 CC required for the identification of pathogens in the clinical laboratory  
 XX  
 SQ Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 U; 0 Other;  
 XX  
 Query Match 99.8%; Score 661.4; DB 4; Length 1837;  
 Best local Similarity 99.8%; Pred. No. 2.1e-120;  
 Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAACAAGACCCCGATCCAGCCCACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 60  
 Db 904 CAACAAGACCCCGATCCAGCCCACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 963  
 QY 61 ATATATTTCTTTATGAGGGTGACCCCTGTACTCACGAGAAATGTGAATCTGTGTGACAA 120  
 Db 964 ATATATTTCTTTATGAGGGTGACCCCTGTACTCACGAGAAATGTGAATCTGTGTGACAA 1023  
 QY 121 CTTTATCTCACCATTAT 180  
 Db 1024 CTTTATCTCACCATTAT 1083  
 QY 181 GAATTAAGACCAAGAGATGGCACTTATTTAAGGATATAAAGCTTGTATATATATATAT 240  
 Db 1084 GAATTAAGACCAAGAGATGGCACTTATTTAAGGATATAAAGCTTGTATATATATATAT 1143  
 QY 241 GTAGATATATACCATCTCTGTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 300  
 Db 1144 GTAGATATATACCATCTCTGTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1203  
 QY 301 GGAGGGGTACAAATCATGAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAA 360  
 Db 1204 GGAGGGGTACAAATCATGAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAA 1263

361 GTATCAATCGATGCTATCCAAAGCCTATCATTTGATATTTGAAACAAATATAAAAAATGGTA 420  
 1264 GTATCAATCGATGCTATCCAAAGCCTATCATTTGATATTTGAAACAAATATAAAAAATGGTA 1323  
 421 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATATCTTACAGATAATAAGCAACTATAT 480  
 1324 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATATCTTACAGATAATAAGCAACTATAT 1383  
 481 ACTAATGCACTTCTCTAAATATGAAACTGGATATATAAAGTTTCACTACCTAAGATAAGAA 540  
 1384 ACTAATGCACTTCTCTAAATATGAAACTGGATATATAAAGTTTCACTACCTAAGATAAGAA 1443  
 541 AGTTTTGGTTGATTTTTTCCCTGAACCAAGATTTTACTCAATCTAATATATCTTATGATA 600  
 1444 AGTTTTGGTTGATTTTTTCCCTGAACCAAGATTTTACTCAATCTAATATATCTTATGATA 1503  
 601 TATAAAGATAATGAAACGCTTGACTCAACACAGCCAAATTTGAAGTCTACTAACCAACC 660  
 1504 TATAAAGATAATGAAACGCTTGACTCAACACAGCCAAATTTGAAGTCTACTAACCAACC 1563  
 661 AAG 663  
 1564 AAG 1566

RESULT 6  
 AAZ51112  
 ID AAZ51112 standard; DNA; 1837 BP.  
 XX  
 AC AAZ51112;  
 XX  
 DT 05-JUN-2000 (first entry)  
 XX  
 DE Streptococcal pyrogenic exotoxin A (SPE-A) encoding DNA.  
 XX  
 KW Superantigen toxin; SAg; Streptococcal pyrogenic exotoxin A; SPE-A;  
 KW antibacterial; vaccine; WMC class II receptor; T-cell antigen receptor;  
 KW cytosolic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA42;  
 KW diagnosis; treatment; superantigen-associated bacterial infection; ds.  
 XX  
 OS Streptococcus sp.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 914..1569  
 FT tag= a  
 XX product= "Streptococcal pyrogenic exotoxin A (SPE-A)"  
 XX WO200009154-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 13-AUG-1998; 98WO-US016766.  
 XX  
 PR 13-AUG-1998; 98WO-US016766.  
 XX  
 PA (REED-) REED ARMY INST RES WALTER.  
 XX  
 PI Ulrich RG, Olson MA, Bavari S;  
 XX  
 DR WPI; 2000-224177/19.  
 DR P-PSDB; AAY70109.  
 XX  
 PT Nucleic acid encoding superantigen toxin useful as a vaccine and for  
 PT diagnosis of superantigen-associated bacterial infections.  
 XX  
 PS Example 12; Page 92-94; 118pp; English.  
 XX  
 CC The present sequence is the DNA encoding Streptococcal pyrogenic exotoxin  
 CC A (SPE-A), a bacterial superantigen toxin (SAG), used for the formulation  
 CC of SPE-A vaccine SPEA42. The coding region of this SAG toxin is altered  
 CC by site directed mutagenesis, introducing L42R mutation, that results in  
 CC disruption of binding of the toxin to both the MHC class II or T-cell  
 CC antigen receptor. SPE-A has antibacterial and cytostatic activity. This

sequence is useful for the production of SPB-A vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxins and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated bacterial infections

XX  
SQ Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 3; Length 1837;  
Best Local Similarity 99.5%; Pred. No. 8.8e-120;  
Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCAGCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 60  
DB |||||  
QY 904 CAACAAGACCCCGATCCAGCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 963  
DB |||||  
QY 61 ATATATTTTCTTTATGAGGGTGACCTGTTACTCAGAGAAATGTAATCTGTTGATCAA 120  
DB ATATATTTTCTTTATGAGGGTGACCTGTTACTCAGAGAAATGTAATCTGTTGATCAA 1023  
QY 121 CTTTATCTCACCATTAT 180  
DB |||||  
QY 1024 CTTAGATCTCAGGATTTAATATATATATATATATATATATATATATATATATATAT 1083  
DB |||||  
QY 181 GAACTTAAGAACCAAGAGATGCAACTTTATTTAAGGATATAAAGCTTGATTTATGTT 240  
DB |||||  
QY 1084 GAACTTAAGAACCAAGAGATGCAACTTTATTTAAGGATATAAAGCTTGATTTATGTT 1143  
DB |||||  
QY 241 GTAGAAATATACCATCTCTGTTTATTTATGTAAGAAATGCAAGAGAGTGCATGTATCAC 300  
DB |||||  
QY 1144 GTAGAAATATACCATCTCTGTTTATTTATGTAAGAAATGCAAGAGAGTGCATGTATCAC 1203  
QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAGAAAGATGCTGTTAAA 360  
DB |||||  
QY 1204 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAGAAAGATGCTGTTAAA 1263  
QY 361 GATCAATCGATGGTATCCAAAGCTTCATTTGATATTTGAACAAATAAATAAATGGTA 420  
DB |||||  
QY 1264 GATCAATCGATGGTATCCAAAGCTTCATTTGATATTTGAACAAATAAATAAATGGTA 1323  
QY 421 ACTGCTCAAGAAATTAGACTATTAAGTTAGAAATATCTTTACAGATAATAAGCAACTATAT 480  
DB |||||  
QY 1324 ACTGCTCAAGAAATTAGACTATTAAGTTAGAAATATCTTTACAGATAATAAGCAACTATAT 1383  
QY 481 ACTATGACCTTCTAATATATGAAGTGAATATTAAGTTTCACTTCAAGTAATAAGAA 540  
DB |||||  
QY 1384 ACTAATGGACCTTCTAATATATGAAGTGAATATTAAGTTTCACTTCAAGTAATAAGAA 1443  
QY 541 AGTTTGTGTTTGAATTTTCCCTGAACAGAAATTTACTCAATCTAATATCTTATGATA 600  
DB |||||  
QY 1444 AGTTTGTGTTTGAATTTTCCCTGAACAGAAATTTACTCAATCTAATATCTTATGATA 1503  
QY 601 TATAAGATATAGAAACGCTTGACTCAACACAGCAAGCCAAATTTGAAGTCTACCTAACACC 660  
DB |||||  
QY 1504 TATAAGATATAGAAACGCTTGACTCAACACAGCAAGCCAAATTTGAAGTCTACCTAACACC 1563  
QY 661 AAG 663  
DB |||||  
QY 1564 AAG 1566

RESULT 7  
ABN84229  
ID ABN84229 standard; cDNA; 1837 BP.  
XX  
AC ABN84229;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Streptococcal pyrogenic exotoxin A vaccine SPEa42 coding sequence.  
XX  
KW Exotoxin A; SPEa; SPEa42; superantigen; antigen; toxin; vaccine;

attenuation; mutant; gene; ss.  
XX  
OS Streptococcus pyogenes.  
XX  
FH Synthetic.  
XX  
Key Location/Qualifiers  
FT 814..1569  
CDS /\*tag= a  
/\*product= "SPEa42"  
XX  
US6399332-B1.  
XX  
PD 04-JUN-2002.  
XX  
PF 01-SEP-1998; 98US-00144776.  
XX  
PR 25-JUN-1997; 97US-00882431.  
XX  
PA (USSA) US SEC OF ARMY.  
XX  
PI Ulrich RG, Olson MA, Bavari S;  
XX  
XX WPI; 2002-546281/58.  
DR P-PSDB; 38879508.  
XX  
XX Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases.  
XX  
PS Disclosure; Col 61-63; 46pp; English.  
XX  
CC The present sequence is the coding sequence of Streptococcus pyogenes vaccine SPEa42. The vaccine differs from the native SPEa sequence by substitution of the Leu-42 residue by Arg. This mutation is expected to disrupt contact between the toxin and the HLA-DR receptor, reducing DRI binding. SPEa42 can be expressed as a recombinant protein in Escherichia coli as a secreted protein or as a cytoplasmic product. No indicators of toxicity have been detected for the purified recombinant protein, and vaccine studies demonstrate that SPEa42 is highly antigenic, inducing protective immunity in a mouse animal model. The attenuated superantigen can be used to protect against superantigen toxin infections. Methods of producing and using altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided by the invention. A multivalent vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1, TSSP-1 and SPEa is predicted to provide protective immunity against the majority of bacterial superantigen toxins  
XX  
SQ Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 6; Length 1837;  
Best Local Similarity 99.5%; Pred. No. 8.8e-120;  
Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCAGCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 60  
DB |||||  
QY 904 CAACAAGACCCCGATCCAGCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 963  
DB |||||  
QY 61 ATATATTTTCTTTATGAGGGTGACCTGTTACTCAGAGAAATGTAATCTGTTGATCAA 120  
DB ATATATTTTCTTTATGAGGGTGACCTGTTACTCAGAGAAATGTAATCTGTTGATCAA 1023  
QY 121 CTTTATCTCACCATTAT 180  
DB |||||  
QY 1024 CTTAGATCTCAGGATTTAATATATATATATATATATATATATATATATATATATAT 1083  
DB |||||  
QY 181 GAACTTAAGAACCAAGAGATGCAACTTTATTTAAGGATATAAAGCTTGATTTATGTT 240  
DB |||||  
QY 1084 GAACTTAAGAACCAAGAGATGCAACTTTATTTAAGGATATAAAGCTTGATTTATGTT 1143  
DB |||||  
QY 241 GTAGAAATATACCATCTCTGTTTATTTATGTAAGAAATGCAAGAGAGTGCATGTATCAC 300  
DB |||||  
QY 1144 GTAGAAATATACCATCTCTGTTTATTTATGTAAGAAATGCAAGAGAGTGCATGTATCAC 1203

QY 301 GGAGGGTAAACAAATCATGAAGGGAATCATTTAGAAAATTCCTAAAGAGATAGTCGTTAAA 360  
Db 1204 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAAATTCCTAAAGAGATAGTCGTTAAA 1263  
QY 361 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATTAATAAATGGTA 420  
Db 1264 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATTAATAAATGGTA 1323  
QY 421 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATCTTACAGATAATAAGCAACTATAT 480  
Db 1324 ACTGCTCAAGAAATAGACTATATAAGTTAGAAAATCTTACAGATAATAAGCAACTATAT 1383  
QY 481 ACTAATGACCTCTTAAATATGAACACTGGATATATAAAGTTTCATACCTTAAGATAAAGAA 540  
Db 1384 ACTAATGACCTCTTAAATATGAACACTGGATATATAAAGTTTCATACCTTAAGATAAAGAA 1443  
QY 541 AGTTTGGTTGATTTTTCCCTGAACCAAGAAATTTACTCAATCTAAATATCTTATGATA 600  
Db 1444 AGTTTGGTTGATTTTTCCCTGAACCAAGAAATTTACTCAATCTAAATATCTTATGATA 1503  
QY 601 TATAAGATAATGAACCTTGAACCTCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 660  
Db 1504 TATAAGATAATGAACCTTGAACCTCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1563  
QY 661 AAG 663  
Db 1564 AAG 1566

## RESULT 8

ACA61184  
ID ACA61184 standard; DNA; 1837 BP.

AC ACA61184;

11-AUG-2003 (first entry)

DNA encoding streptococcal pyrogenic exotoxin A.

Pyrogenic exotoxin A; ds; superantigen-associated bacterial infection;  
superantigen toxin; gene; vaccine.

Streptococcus sp.

Key Location/Qualifiers  
CDS 814..1569

/\*tag= a  
/product= "Pyrogenic exotoxin A"

US2003009015-A1.

09-JAN-2003.

25-JUN-1997; 97US-00882431.

25-JUN-1997; 97US-00882431.

(ULRI/) ULRICH R G.

(OLSO/) OLSON M A.

(BAVA/) BAVARI S.

Ulrich RG, Olson MA, Bavari S;

WPI; 2003-401542/38.

P-PSDB; ABU10088.

New superantigen toxin and/or DNA fragment with an altered binding of the  
encoded altered toxin to either MHC class II or T cell antigen receptor,  
useful for treating or ameliorating superantigen-associated bacterial  
infection.

Claim 9; Page 32-34; 50pp; English.

CC The invention relates to an isolated and purified superantigen toxin  
CC and/or DNA fragment, which has been altered so that the binding of the  
CC encoded toxin to either major histocompatibility complex (MHC) class II  
CC or T cell antigen receptor is altered. The superantigen toxins, DNA  
CC fragments, and vaccines are useful for treating or ameliorating  
CC superantigen-associated bacterial infection. The DNA fragments are  
CC particularly useful for producing vaccine against superantigen toxin  
CC infections. The transformed host cells are useful for analysing the  
CC effectiveness of drugs and agents that affect the binding of  
CC superantigens to MHC class II or T-cell antigen receptors. The present  
CC sequence represents DNA encoding streptococcal pyrogenic exotoxin A  
XX

SQ Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 7; Length 1837;

Best Local Similarity 99.5%; Pred. No. 8.8-120;

Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAAGACCCCGATCCAAAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 60

Db 904 CAACAAGACCCCGATCCAAAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 963

QY 61 ATATATTTTCTTTATGAGGGTGACCCCTGTACTCACGAGATGTGAATCTGTTGATCAA 120

Db 964 ATATATTTTCTTTATGAGGGTGACCCCTGTACTCACGAGATGTGAATCTGTTGATCAA 1023

QY 121 CTTTATCTCACCATTAAATATATAATGTTTCAGGGCCAAATTAATGATAATTAATAACT 180

Db 1024 CTTAGATCTCAGATTTAAATATATAATGTTTCAGGGCCAAATTAATGATAATTAATAACT 1083

QY 181 GAACCTTAAGACCAAGAGATGGCACTTTATTAAGGATAAAGACCTTGATTTATGGT 240

Db 1084 GAACCTTAAGACCAAGAGATGGCACTTTATTAAGGATAAAGACCTTGATTTATGGT 1143

QY 241 GTAGATATTAACCATCTCTGTTATTTATGTGAAATGCAGAAAGAGTGCAATGATCTAC 300

Db 1144 GTAGATATTAACCATCTCTGTTATTTATGTGAAATGCAGAAAGAGTGCAATGATCTAC 1203

QY 301 GGAGGGTAAACAAATCAATGAAGGGAATCATTTAGAAAATTCCTAAAGAGATAGTCGTTAAA 360

Db 1204 GGAGGGTAAACAAATCAATGAAGGGAATCATTTAGAAAATTCCTAAAGAGATAGTCGTTAAA 1263

QY 361 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAGAAATGGTA 420

Db 1264 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATAAAGAAATGGTA 1323

QY 421 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATAT 480

Db 1324 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATAT 1383

QY 481 ACTAATGGACCTTCTAAATATGAACCTGGATATATAAAGTTCTATACCTAAGATAAAGAA 540

Db 1384 ACTAATGGACCTTCTAAATATGAACCTGGATATATAAAGTTCTATACCTAAGATAAAGAA 1443

QY 541 AGTTTTGGTTGATTTTTCCCTGAACCAAGATTTTACTCAATCTAATATCTTATGATA 600

Db 1444 AGTTTTGGTTGATTTTTCCCTGAACCAAGATTTTACTCAATCTAATATCTTATGATA 1503

QY 601 TATAAAGATAATGAACCTGTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCAACC 660

Db 1504 TATAAAGATAATGAACCTGTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCAACC 1563

QY 661 AAG 663

Db 1564 AAG 1566

## RESULT 9

AAD56771

ID AAD56771 standard; DNA; 1837 BP.

XX

AC AAD56771;

XX

06-OCT-2003 (first entry)

Streptococcus pyogenes pyrogenic exotoxin A (SpeA) DNA.

Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA; gene therapy; gene; ds.

Streptococcus pyogenes.

Key: Location/Qualifiers  
CDS 814..1566  
/product= "Streptococcus pyogenes SpeA protein"  
/tag= a  
/transl\_except= (pos:901..903, aa:Met)  
/note= "This translational exception occurs only when decoding SSQ ID NO: 26 (AAE37687)"

sig\_peptide 814..900  
/tag= b

mat\_peptide 901..1566  
/tag= c  
/product= "Streptococcus pyogenes mature SpeA protein"

WO2003056015-A1.

10-JUL-2003.

26-NOV-2001; 2001WO-US046540.

26-NOV-2001; 2001US-00002784.

(USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

Ulrich RG;

WPI; 2003-492125/46.

P-PSDB; AAE37683, AAE37687

New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.

Claim 4; Page 128-129; 141pp; English.

The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin A (SpeA) DNA. This sequence is used in the invention

Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 8; Length 1837;  
Best Local Similarity 99.5%; Pred. No. 8.e-120;  
Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAACAGCCCGATCCAGCCCACTTCACAGATCTAGTTTAAACCTTCAAAAT 60  
2 CAACAGCCCGATCCAGCCCACTTCACAGATCTAGTTTAAACCTTCAAAAT 63  
3 ATATATTTTCTTATGAGGTGACCTGTACTCAGAGAAATGTGAAATCTGTGATCAA 120  
4 ATATATTTTCTTATGAGGTGACCTGTACTCAGAGAAATGTGAAATCTGTGATCAA 1023  
5 CTTTATCTCAGCATTTAT 180  
6 CTTAGATCTCAGCATTTAT 1083  
7 GAACCTTAAGAACCAAGAGATGCACTTTATTTAAGGATAAAACCTGTATATATGTT 240  
8 GAACCTTAAGAACCAAGAGATGCACTTTATTTAAGGATAAAACCTGTATATATGTT 1143  
9 GTAGAATATTACCATCTCTTTATTTATGTGAAATGCAAGAGGAGTGCATGTATCTAC 300

1144 GTAGAATATTACCATCTCTGTTTATTTATGTGAAATGCAAGAGGAGTGCATGTATCTAC 1203

301 GGAGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCTGTTAAA 360

1204 GGAGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCTGTTAAA 1263

361 GTATCAATCGATGGTATCCAAAGCCTCATCTTTGATATTTGAAACAAATAAAAAATGGTA 420

1264 GTATCAATCGATGGTATCCAAAGCCTCATCTTTGATATTTGAAACAAATAAAAAATGGTA 1323

421 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAATATCTTACAGATAAATAAGCAACTATAT 480

1324 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAATATCTTACAGATAAATAAGCAACTATAT 1383

481 ACTAATGACCTCTTAATATGAACCTGATATATAAGTTTCACTAAAGTTCATAGTAAGAAAGAA 540

1384 ACTAATGACCTCTTAATATGAACCTGATATATAAGTTTCACTAAAGTTCATAGTAAGAAAGAA 1443

541 AGTTTTTGGTTTGAATTTTCCCTGAACGAGAAATTTACTCAATCTAAATATCTTATGATA 600

1444 AGTTTTTGGTTTGAATTTTCCCTGAACGAGAAATTTACTCAATCTAAATATCTTATGATA 1503

601 TATAAGATAATGAACGCTTGAATCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 660

1504 TATAAGATAATGAACGCTTGAATCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1563

661 AAG 663

1564 AAG 1566

RESULT 10

ACD28901

ID ACD28901 standard; DNA; 1837 BP.

XX

AC ACD28901;

XX

DT 27-AUG-2003 (first entry)

XX

DE Streptococcus pyrogenic toxin a L42R mutant, DNA.

XX

SW SpeA; streptococcus pyrogenic enterotoxin a; gene; mutant; vaccine; ds;  
KW superantigen toxin; MHC; superantigen-associated bacterial infection;  
KW bacterial infection; antibacterial.

XX

OS Streptococcus sp.

OS Synthetic.

XX

Key Location/Qualifiers

FT CDS 814..1566

FT /tag= a

FT /product= "SpeA L42R"

FT sig\_peptide 814..903

FT /tag= b

FT mat\_peptide 904..1566

FT /tag= c

FT /label= Mature\_SPEA\_L42R

XX

PN US2003036544-A1.

XX

20-FEB-2003.

XX

26-NOV-2001; 2001US-00002784.

XX

25-JUN-1997; 97US-00882431.

XX

01-SEP-1998; 98US-00144776.

XX

ULRI (/) ULRICH R G.

XX

ULRI RG;

XX

WPI; 2003-792125/46

DR P-PSDB; ABU62331.

XX New superantigen toxin DNA fragment, useful for preparing a composition

PT for treating or preventing bacterial infection.

PS Claim 4; Page 36-37; 68pp; English.

XX The invention relates to an isolated and purified superantigen toxin DNA

CC fragment is altered so that binding of the encoded altered toxin to

CC either the MHC class II or T cell antigen receptor is altered. Also

CC included are a recombinant DNA construct (comprising a vector and an

CC isolated and purified altered superantigen toxin DNA fragment), a host

CC cell transformed with the recombinant DNA construct, producing altered

CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)

CC superantigen toxin peptide, diagnosing superantigen-associated bacterial

CC infection, a vaccine (comprising an altered superantigen toxin for

CC producing antigenic and immunogenic response resulting in the protection

CC of a mammal against superantigen-associated bacterial infection),

CC treating/ameliorating a superantigen-associated bacterial infection,

CC antiserum isolated from individuals immunised with one or more altered

CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-

CC SEB, SECI) and streptococcal pyrogenic enterotoxin A, B, Cl (SEA,

CC SPEb). The superantigen toxin DNA fragment is useful for preparing a

CC composition for treating or preventing bacterial infection. The present

CC sequence encodes the L42R (with reference to the mature protein) mutant

CC of SPEa

XX

SQ Sequence 1837 BP; 633 A; 318 C; 248 G; 638 T; 0 U; 0 Other;

Query Match 99.0%; Score 656.6; DB 8; Length 1837;

Best Local Similarity 99.4%; Pred. No. 1.8e-119;

Matches 659; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACACAGACCCGATCCAGCAACTTCACAGACTCTAGTTAGTTAAACCTTCAAAAT 60

Db 904 CAACAGACCCGATCCAGCAACTTCACAGACTCTAGTTAGTTAAACCTTCAAAAT 963

QY 61 ATATATTTCTTTATGAGGTGACCTGTTACTACAGAGATGTGAATCTGTGTATCAA 120

Db 964 ATATATTTCTTTATGAGGTGACCTGTTACTACAGAGATGTGAATCTGTGTATCAA 1023

QY 121 CTTTATCTCACCATTAAATATATTAATGTTTCAGGCGCAATATATGATAATTAATAA 180

Db 1024 CTTAGATCTCAGATTAAATATATTAATGTTTCAGGCGCAATATATGATAATTAATAA 1083

QY 181 GAACCTTAAGACCAAGAGATGGCACTTTATTAAGGATAAAACGTTGATATTTATGGT 240

Db 1084 GAACCTTAAGACCAAGAGATGGCACTTTATTAAGGATAAAACGTTGATATTTATGGT 1143

QY 241 GTAGATATTTACCATCTCTGTTATTTATGTAAGTGCAGAAAGGAGTGCATGTATCTAC 300

Db 1144 GTAGATATTTACCATCTCTGTTATTTATGTAAGTGCAGAAAGGAGTGCATGTATCTAC 1203

QY 301 GGAGGGGTAAACAATCATGAAGGGAATCATTTAGAAATTCCTAAAGATAGTGGTTAAA 360

Db 1204 GGAGGGGTAAACAATCATGAAGGGAATCATTTAGAAATTCCTAAAGATAGTGGTTAAA 1263

QY 361 GTATCAATCATGATGTATCCAAAGCCTATCATTTGATATTCAGAAACAAATAAAAAATGGTA 420

Db 1264 GTATCAATCATGATGTATCCAAAGCCTATCATTTGATATTCAGAAACAAATAAAAAATGGTA 1323

QY 421 ACTGCTCAAGAAATAGACTATTAAGTTAGAAATATCTTACAGATATTAAGCAACTATAT 480

Db 1324 ACTGCTCAAGAAATAGACTATTAAGTTAGAAATATCTTACAGATATTAAGCAACTATAT 1383

QY 481 ACTAATGGACCTTCTAAATATGAAGTGGATATATAAAGTTCTACCTTAAGATAAGAA 540

Db 1384 ACTAATGGACCTTCTAAATATGAAGTGGATATATAAAGTTCTACCTTAAGATAAGAA 1443

QY 541 AGTTTGGTTGGTTGTTTTTCCCTGGAACCAAGATTTACTCAATCTAAATATCTTATGATA 600

Db 1444 AGTTTGGTTGGTTGTTTTTCCCTGGAACCAAGATTTACTCAATCTAAATATCTTATGATA 1503

QY 601 TATAAGATATGAACGCTTGACTCAAAACACAGCCAAATGAAGTCTCCTTAACCAACC 660

Db 1504 TATAAGATATGAACGCTTGACTCAAAACACAGCCAAATGAAGTCTCCTTAACCAACC 1563

QY 661 AAG 663

Db 1564 AAG 1566

RESULT 11

ACD28908

ID ACD28908 standard; DNA; 1419 BP.

XX ACD28908;

XX 27-AUG-2003 (first entry)

DE SPEa L42R/SPEb C47S mutant fusion protein, DNA.

XX SPEa; streptococcus pyrogenic enterotoxin; gene; mutant; vaccine; ds;

XX superantigen toxin; MHC; superantigen-associated bacterial infection;

XX bacterial infection; antibacterial; SPEb.

OS Streptococcus sp.

OS Synthetic.

PH Key Location/Qualifiers

FT CDS 1. 1419

FT /tag= a

FT /product= "SPEa L42R/SPEb C47S"

FT /transl\_except= (pos:298..306,aa:Ile-Gly)

FT /transl\_except= (pos:634..642,aa:Thr-Gln)

FT /transl\_except= (pos:1162..1170,aa:Ser-Gln)

FT /transl\_except= (pos:1228..1236,aa:Gly-Gly)

XX US2003036644-A1.

XX 20-FEB-2003.

XX 26-NOV-2001; 2001US-00002784.

XX 25-JUN-1997; 97US-00882431.

XX 01-SEP-1998; 98US-00144776.

XX (ULRI/) ULRICH R G.

XX Ulrich RG;

XX WPI; 2003-492125/46.

XX P-PSDB; ABU62335.

XX New superantigen toxin DNA fragment, useful for preparing a composition

XX for treating or preventing bacterial infection.

XX Claim 6; Page 39-40; 68pp; English.

XX The invention relates to an isolated and purified superantigen toxin DNA

XX fragment is altered so that binding of the encoded altered toxin to

XX either the MHC class II or T cell antigen receptor is altered. Also

XX included are a recombinant DNA construct (comprising a vector and an

XX isolated and purified altered superantigen toxin DNA fragment), a host

XX cell transformed with the recombinant DNA construct, producing altered

XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)

XX superantigen toxin peptide, diagnosing superantigen-associated bacterial

XX infection, a vaccine (comprising an altered superantigen toxin for

XX producing antigenic and immunogenic response resulting in the protection

XX of a mammal against superantigen-associated bacterial infection),

XX treating/ameliorating a superantigen-associated bacterial infection, an

XX antiserum isolated from individuals immunised with one or more altered

XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-

XX 1. Also disclosed are mutated streptococcal enterotoxin A, B, Cl (SEA,

XX SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and

CC	SPEB). The superantigen toxin DNA fragment is useful for preparing a
CC	composition for treating or preventing bacterial infection. The present
CC	sequence encodes the SpeA L42R/SPEB C47S mutant fusion protein
XX	
SQ	Sequence 1419 BP; 497 A; 266 C; 255 G; 401 T; 0 U; 0 Other;
Query Match.	
Best Local Similarity 98.3%; Score 651.8; DB 8; Length 1419;	
Matches 656; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
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Dd	
Dd	4 CAACAAGACCCGATCCAAGCCAACTTCACAGATCTAGTTTGGTTAGTTAAAAACCTTCAAAAT 63
Qy	61 ATATATTCTTTTAAGAGGTGACCCCTGTACTCACGAGAATGGAATCTGTGTATCAAA 120
Dd	
Dd	64 ATATATTCTTTTAAGAGGTGACCCCTGTACTCACGAGAATGGAATCTGTGTATCAAA 123
Qy	121 CTTTTACTCACCATTAAATAATAAAGTTTCAGGGCCAAATTATGATAAAATTTAAAAC 180
Dd	
Dd	124 CTTCGATCTCACGATTTAATAATAAAGTTTCAGGGCCAAATTATGATAAAATTTAAAAC 183
Qy	181 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATNAAAAACGTTTGATATTATGGT 240
Dd	
Dd	184 GAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATNAAAAACATTTGATATTATGGT 243
Qy	241 GTAGAAATTTACCATCTCTGTTNTTATGTGAAAATGCAGAAAGAGTGATGTATCTAC 300
Dd	
Dd	244 GTAGAAATTTACCATCTCTGTTNTTATGTGAAAATGCAGAAAGAGTGATGTATCTAC 303
Qy	301 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAAATTCCTTAAAAAGATAGTCGTTAAA 360
Dd	
Dd	304 GGAGGGGTAAACAAATCGTAGAGGGAATCATTTAGAAAATTCCTTAAAAAGATAGTCGTTAAA 363
Qy	361 GTATCAATCGATGGTATCCAAAGCCATCATTTGATTTGAAAACAAATAAAAAAATGGTA 420
Dd	
Dd	364 GTATCAATCGATGGTATCAAAAGCCATCATTTGATTTGAAAACAAATAAAAAAATGGTA 423
Qy	421 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATAT 480
Dd	
Dd	424 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATAT 483
Qy	481 ACTAATGGACCTTCTAAATATGAAACTGGATATATAAAGTTTCATACCTPAAGAAATAAGAA 540
Dd	
Dd	484 ACTAATGGACCTTCTAAATATGAAACTGGATATATAAAGTTTCATACCTPAAGAAATAAGAA 543
Qy	541 AGTTTTTGGTTGGATTTTTTCCCTGACCCAGAAATTTACTCAATCTTAATATCTTATGATA 600
Dd	
Dd	544 AGTTTTTGGTTGGATTTTTTCCCTGACCCAGAAATTTACTCAATCTTAATATCTTATGATA 603
Qy	601 TATAAAGATATGAACCGCTTGACTCAAAACCAAGCCAAATTTGAAGTCTACTCAACACC 660
Dd	
Dd	604 TATAAAGATATGAACCGCTTGACTCAAAACCAAGCCAAATTTGAAGTCTACTCAACACC 663
Qy	661 AAG 663
Dd	
Dd	664 AAG 666
RESULT 12	
AAD56778	
ID	AAD56778 standard; DNA; 1419 BP.
XX	
AC	
XX	AAD56778;
XX	
DT	06-OCT-2003 (first entry)
XX	
DE	Streptococcus pyogenes SpeA-SpeB fusion DNA.
XX	
KW	Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
Kw	gene therapy; fusion protein; SpeB; gene; ds.
XX	
XS	Streptococcus pyogenes.



QY 421 ACTGCTCAAGATTAGACTATATAAGTTAGAAAATATCTTACAGATAATAAGCAACTATAT 480  
 Db |||||  
 QY 424 ACTGCTCAAGATTAGACTATATAAGTTAGAAAATATCTTACAGATAATAAGCAACTATAT 483  
 Db |||||  
 QY 481 ACTATGACCTTCTAATATGAACTGATATATAAAGTTCCATACCTAAGATAAAGAA 540  
 Db |||||  
 QY 484 ACTAATGACCTTCTAATATGAACTGATATATAAAGTTCCATACCTAAGATAAAGAA 543  
 Db |||||  
 QY 541 AGTTTTCGTTGATTTTTCCTCGAACCCAGAAATTTACTCAATCTAATATCTTATGATA 600  
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 QY 544 AGTTTTCGTTGATTTTTCCTCGAACCCAGAAATTTACTCAATCTAATATCTTATGATA 603  
 Db |||||  
 QY 601 TATAAGATAATGAACGCTTGACTCAACACAGCCAAATGGAAGTCTACCTAACCAACC 660  
 Db |||||  
 QY 604 TATAAGATAATGAACGCTTGACTCAACACAGCCAAATGGAAGTCTACCTAACCAACC 663  
 QY 661 AAG 663  
 Db |||||  
 QY 664 AAG 666

## RESULT 13

ACA64700  
 ID ACA64700 standard; DNA; 1031 BP.

AC ACA64700;

DT 18-JUN-2003 (first entry)

DE S. Pyogenes exotoxin (SPEA) gene.

KW Superantigen; ds; gene; SAG; staphylococcal enterotoxin; tumour; cancer;  
 KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;  
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;  
 KW tumouricidal immunocyte; anti-tumour.

OS Streptococcus pyogenes.

XX US2002177551-A1.

XX 28-NOV-2002.

XX 30-MAY-2001; 2001US-00870759.

XX 31-MAY-2000; 2000US-0208128P.

XX (TERM/) Terman D S.

PA Terman DS;

XX WPI; 2003-361759/34.

XX P-PSDB; ABU79074.

PT A mammalian cell receptor, useful in the treatment of cancer by binding  
 PT to tumor associated lipids where the binding induces anergy or apoptosis  
 XX in T cells and antigen presenting cells.

PS Disclosure; Page: 167pp; English.

XX The invention relates to a mammalian cell receptor, useful in the  
 CC treatment of cancer, which binds to tumour associated lipids and induces  
 CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).  
 CC Also included are a mammalian cell useful in the treatment of cancer  
 CC where the receptor which binds tumour associated lipids and induces  
 CC cellular inactivation or death is deleted or functionally deactivated,  
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal  
 CC (by allowing tumour associated lipids to contact immunocytes in which  
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,  
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,  
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or  
 CC deleted); a construct useful in the treatment of cancer comprising a  
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell  
 CC useful in the treatment of cancer (where an adaptor protein which

CC inhibits T cell activation by tumour associated antigens is deleted or  
 CC functionally deactivated), a composition useful in the treatment of  
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing  
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by  
 CC allowing tumour associated lipids to contact immunocytes, in which  
 CC receptors for the lipids are inactivated or deleted to produce a  
 CC tumouricidal immunocyte population, and administering the tumouricidally  
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC  
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to  
 CC contact APCs, in which receptors for the tumour associated lipids are  
 CC inactivated or deleted to produce a tumouricidally activated population,  
 CC and administering APCs to the host), producing a tumouricidal T cell  
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to  
 CC contact T cells, in which adaptor proteins, which inhibit T cell  
 CC activation by tumour associated antigens, are deleted or functionally  
 CC deactivated to produce a tumouricidal population of T cells, and  
 CC administering the tumouricidally activated T cells to the host, or  
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and  
 CC administering the tumouricidally activated T cells to the host), treating  
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which  
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)  
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a  
 CC tumour associated antigen to contact immunocytes in which adaptor  
 CC proteins which inhibit T cell activation by tumour associated antigens  
 CC are deleted or functionally deactivated) and producing (M7) a  
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a  
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The  
 CC receptors, methods and compositions are useful for treating cancers and  
 CC tumours. Bacterial superantigens are co-administered or administered as  
 CC fusion constructs with anti-tumour proteins or motifs. The present  
 CC sequence encodes a bacterial superantigen protein (e.g. a staphylococcal  
 CC enterotoxin). Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format from  
 CC the US patent office website at  
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"

XX Sequence 1031 BP; 381 A; 146 C; 162 G; 342 T; 0 U; 0 Other;

Query Match 87.9%; Score 582.6; DB 7; Length 1031;

Best Local Similarity 97.1%; Pred. No. 5.3e-105;

Matches 636; Conservative 0; Mismatches 14; Indels 5; Gaps 4;

QY 10 CCGGATCCAGCCCAACTTCCAGATCTAGTTAGTTAAACCTTCAAAATATATATTTT 69  
 Db |||||  
 QY 178 CCCAAGCCCGCCCAATACAAAGATCTAATTTAGTT-AAAACCTTCAAAATATATATTTT 236  
 Db |||||  
 QY 70 CTTTATGAGGGTGACCCCT-GTTACTCAGAGAAATGTGAAATCTGTGATCAACTTTTATC 128  
 Db |||||  
 QY 237 CTTTATGAGGGTGACCCCTGTTACTCAGAGAAATGTGAAATCTGTGATCAACTTTTATC 296  
 QY 129 TCACCATTTAATATATAATGTTTCAGGGCCAAATTTATGATAAAATATAAACTGAACCTAA 188  
 Db |||||  
 QY 297 ACAGATTTAATATATAATGTTTCAGGGCCAAATTTATGATAAAATATAAACTGAACCTAA 356  
 QY 189 GAACCAAGAGATGGCACTTTATTTAGGATAAAACGTTGATATTTTATGGTAGAATA 248  
 Db |||||  
 QY 357 GAACCAAGAGATGGCACTTTATTTAGGATAAAACGTTGATATTTTATGGTAGAATA 416  
 QY 249 TTACCATCTCTGTTATTTATGTGAAAATGAGAGAGTGCATGTATCTACGAGGGGT 308  
 Db |||||  
 QY 417 TTACCATCTCTGTTATTTATGTGAAAATGAGAGAGTGCATGTATCTACGAGGGGT 476  
 QY 309 AACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAAGATAGTCGTTAAAGTATCAAT 368  
 Db |||||  
 QY 477 AACAAATCATGAAGGGAATCATTTAGAAATTCCTAAAAGATAGTCGTTAAAGTATCAAT 536  
 QY 369 CGATGGTATCCAAAGCCTATCTTATGATTTGAAACAAATATAAAATATGTAATCTGCTCA 428  
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 QY 537 CGATGGTATCCAAAGCCTATCTTATGATTTGAAACAAATATAAAATATGTAATCTGCTCA 594  
 QY 429 AGAATTAGACTATAAAAGTTAGAAAATATCTTACAGATAATAACCAACTATATATACTATGG 488  
 Db |||||  
 QY 595 AGAATTAG-CTATACAGTTAGAAAATATCTTACAGATAATAACCAACTATATATACTATGG 653



Db 803 CTGACACAGCGCATAAGTTTGACCAATCTAAATATTTAATGATGTACACGACATATAAA 862  
 QY 617 CGCTTGACTCAACACACAGCCAAATTTGAAGTCTACCTAACACCAAG 663  
 Db 863 CGGTGTGATTCTAAAGTGTGAAGATAGAGTCCACCTTACACCAAG 909  
 RESULT 15  
 AAT45698  
 ID AAT45698 standard; cDNA; 773 BP.  
 XX  
 AC AAT45698;  
 XX  
 DT 08-MAR-1997 (first entry)  
 XX  
 DE Staphylococcus enterotoxin B cDNA.  
 XX  
 KW Enterotoxin B; SEB; superantigen; antigen; cytokine; chemokine; T cell;  
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;  
 KW adjuvant; ss.  
 XX  
 OS Staphylococcus sp.  
 XX  
 FH Location/Qualifiers  
 FT CDS 1..768  
 FT /\*tag= a  
 FT /note= "the full-length coding sequence can be used in  
 FT nucleic acid-based therapeutic compsns. of the invention"  
 FT 1..45  
 FT sig\_peptide  
 FT /\*tag= b  
 FT complement (37..61)  
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 FT /note= "SEB.S amplification primer binding site"  
 FT 46..765  
 FT mat\_peptide  
 FT /\*tag= c  
 FT /note= "the coding sequence for the mature protein can be  
 FT used in nucleic acid-based therapeutic compsns. of the  
 FT invention"  
 FT 754..768  
 FT primer\_bind  
 FT /\*tag= e  
 FT /note= "SEB.S amplification primer binding site"  
 FT  
 XX WO9636366-A1.  
 XX  
 XX 21-NOV-1996.  
 XX  
 XX 20-MAY-1996; 96WO-US007432.  
 XX  
 XX 18-MAY-1995; 95US-00446918.  
 XX 29-DEC-1995; 95US-00580806.  
 XX  
 XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.  
 XX  
 XX Dow SW, Elmslie RE, Potter TA;  
 XX WPI; 1997-011857/01.  
 XX P-PSDB; AAW06737.  
 XX  
 XX Recombinant molecule encoding superantigen and opt. cytokine or  
 XX chemokine - controls activity of effector cells (T cells, monocytes,  
 XX natural killer cells), used for gene therapy of cancer.  
 XX  
 XX Example 1; Page 95-96; 131pp; English.  
 XX  
 XX A cDNA clone (AAT45698) codes for staphylococcal enterotoxin B (AAW06737)  
 XX superantigen. Nucleic acids encoding superantigens (see also AAT45699 and  
 XX AAT45706) can be utilised in the gene therapy of cancer, infectious  
 XX diseases and immunological disorders. The nucleic acid, optionally in  
 XX combination with cytokine or chemokine nucleic acids, is delivered to an  
 XX animal using e.g. liposomes. It acts by controlling the activity of  
 XX effector cells, such as T-cells, macrophages, monocytes and/or natural  
 XX killer cells. Localised prodn. of an effective but non-toxic amount of  
 XX encoded proteins allows safe treatment of the animal. Adjuvants

CC comprising an immunogen and a superantigen nucleic acid can be used with  
 CC DNA-based vaccines  
 XX  
 SQ Sequence 773 BP; 305 A; 94 C; 133 G; 241 T; 0 U; 0 Other;  
 Query Match 25.2%; Score 166.8; DB 2; Length 773;  
 Best Local Similarity 59.1%; Pred. No. 1.3e-23;  
 Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;  
 QY 56 AAAATATATATTTCTTTTATGAGGCTGACCTGTTACTCAGGAAATGTGAAATCTGTTG 115  
 Db 113 AAAATATGAAAGTTTGTATGATGATATCATGTATCAGCAATAAACCTTAAATCTATAG 172  
 QY 116 ATCAACTTTTATCTCACCAATTTAATATATATATGTTTCAGGGCCA-----AATTATG 166  
 Db 173 ATCAATTTCTATCTTTGACTTAAATATCTTATTAAGGACACTAAGTTAGGGAATTATG 232  
 QY 167 ATAAATTAATAAAGCTTAAGTAAGCAAGAGATGGCAACTTTTATTTAAGGATATAAACG 226  
 Db 233 ATAATGTTTCGAGTCGAATTTTAAACCAAGATTTAGCTGATATAATACAAAGATAAATACG 292  
 QY 227 TTGATATTTATGGTGTAGAAATATTACCATCTCTCTTATTTATGTGAAAA----- 275  
 Db 293 TAGATGTTTGGAGCTAATTTATTTATCAATGTTATTTTCTTAAAAAACGATGNTA 352  
 QY 276 -----TGCAGAAAGGAGTGATGTATCTACGAGGGGTAAACAAATTAGACT 439  
 Db 353 TTAATTCGCATCAAACTGACAAACGAAAACTTGATGTATGTTGTTAACTGAGCATA 412  
 QY 320 AAGGGAATCATTTAGAAATTCCTAAAAAGATAGTCGTTAAAGTATCAATCATGATGATCC 379  
 Db 413 ATGGAACCAATTAGATAAATATAGAAATTTACTGTTGGGTATTTGAAGATGTTAAAA 472  
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 Db 473 ATTTATTTCTTTTGACGTACAACTAATTAAGAAAAAGGTGACCTCAAGATTAGATT 532  
 QY 440 ATAAAGTTAGAAATATCTTTACAGATAATAAGCAACTATATATACTAAATGGACCTTCTAAAT 499  
 Db 533 ACCTAACTCGTCACTATTTGGTAAAAATAAAAACTCTATGAATTTTAAACAACTCGCTT 592  
 QY 500 ATGAAACTGGATATATAAAGTTCATACCTAAGATAAAGAAAGTTTGGTTTCATTTT 559  
 Db 593 ATGAAACGGATATATTAAATTTTAAATTAATA-----GAAATGAGATAGCTTTGGTATGACATGA 649  
 QY 560 TCCTGAACCAAG-----AAATTTACTCAATCTAAATATCTTATGATATATAAGATATG 613  
 Db 650 TGCTGCACCAAGAGATAAATTTGACCAATCTAAATATTTAATGATGTACATGACATA 709  
 QY 614 AAAGCTTGACTCAACACAAAGCCAAATTTGAAGTCTACCTAACCAACCAAG 663  
 Db 710 AAATGGTTGATCTTAAAGATGTGAAGATTGAAGTTTATCTTACGACAAAG 759  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
7809.322 Million cell updates/sec

Title: US-10-625-221-12\_COPY\_918\_1580

Perfect score: 663

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3267054 seqs, 2485319735 residues

Total number of hits satisfying chosen parameters: 6534108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
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9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
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11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10C\_NEW\_PUB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	1851	8	US-08-973-391A-12
2	663	100.0	1851	13	US-09-308-830-12
3	661.4	99.8	1837	9	US-09-452-599-33
4	661.4	99.8	1837	15	US-10-121-120-33
5	658.2	99.3	1837	8	US-08-882-431-15
6	656.6	99.0	1837	15	US-10-002-784A-15
7	651.8	98.3	1419	15	US-10-002-784A-23
8	582.6	87.9	1031	9	US-09-870-759-19
9	582.6	87.9	1031	10	US-09-751-708A-19
10	167.4	25.2	1095	9	US-08-870-759-11
11	167.4	25.2	1095	10	US-09-751-708A-11
12	166.8	25.2	773	13	US-10-354-948-1
13	166.8	25.2	801	9	US-09-870-759-1
14	166.8	25.2	801	10	US-09-751-708A-1

15 166.8 25.2 886 9 US-09-870-759-2 Sequence 2, Appli  
16 166.8 25.2 886 10 US-09-751-708A-2 Sequence 2, Appli  
17 166.8 25.2 886 10 US-08-882-431-5 Sequence 5, Appli  
18 166.8 25.2 1712 9 US-09-870-759-9 Sequence 9, Appli  
19 166.8 25.2 1712 10 US-09-751-708A-9 Sequence 9, Appli  
20 166.8 25.2 1712 15 US-10-002-784A-5 Sequence 5, Appli  
21 166.8 25.2 1712 15 US-10-002-784A-5 Sequence 13, Appli  
22 164.2 24.8 1095 8 US-08-882-431-13 Sequence 13, Appli  
23 164.2 24.8 1095 15 US-10-002-784A-13 Sequence 13, Appli  
24 158.8 24.0 723 16 US-10-405-871-3 Sequence 3, Appli  
25 158.8 24.0 801 16 US-10-405-871-2 Sequence 2, Appli  
26 158.8 24.0 1388 8 US-08-882-431-9 Sequence 9, Appli  
27 158.8 24.0 1388 15 US-10-002-784A-9 Sequence 9, Appli  
28 158.8 24.0 1712 8 US-08-882-431-7 Sequence 7, Appli  
29 112 16.9 815 15 US-10-002-784A-7 Sequence 7, Appli  
30 96.6 14.6 1136 9 US-09-870-759-13 Sequence 13, Appli  
31 96.6 14.6 1136 10 US-09-751-708A-13 Sequence 13, Appli  
32 79 11.9 1443 9 US-09-870-759-7 Sequence 7, Appli  
33 79 11.9 1443 10 US-09-751-708A-7 Sequence 7, Appli  
34 71 10.7 757 8 US-08-882-431-3 Sequence 3, Appli  
35 71 10.7 757 15 US-10-002-784A-3 Sequence 3, Appli  
36 71 10.7 774 16 US-10-405-871-1 Sequence 1, Appli  
37 71 10.7 774 9 US-09-870-759-15 Sequence 15, Appli  
38 71 10.7 774 10 US-09-751-708A-15 Sequence 15, Appli  
39 71 10.7 830 8 US-08-882-431-1 Sequence 1, Appli  
40 71 10.7 830 15 US-10-002-784A-1 Sequence 1, Appli  
41 66.2 10.0 675 8 US-08-781-986A-887 Sequence 887, App  
42 66.2 10.0 675 13 US-10-329-624-887 Sequence 887, App  
43 62.2 9.4 1789 9 US-09-939-980-116 Sequence 116, App  
44 60.8 9.2 7597 15 US-10-311-455-986 Sequence 986, App  
c 45 60.6 9.1 3673778 15 US-10-312-841-1 Sequence 1, Appli

## ALIGNMENTS

## RESULT 1

US-08-973-391A-12  
; Sequence 12, Application US/08973391A  
; Publication No. US20020054887A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlievert, Patrick M.  
; APPLICANT: Roggiani, Manuela  
; APPLICANT: Stoehrt, Jennifer  
; APPLICANT: Ohlendorf, Douglas  
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE  
; FILE REFERENCE: 600.311USWO  
; CURRENT APPLICATION NUMBER: US/08/973,391A  
; CURRENT FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: PCT/US96/10252  
; PRIOR FILING DATE: 1996-06-07  
; PRIOR APPLICATION NUMBER: US 08/480,261  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 1851  
; TYPE: DNA  
; ORGANISM: Streptococcus pyogenes  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (828)..(1583)  
; OTHER INFORMATION:  
US-08-973-391A-12

Query Match 100.0%; Score 663; DB 8; Length 1851;

Best Local Similarity 100.0%; Pred. No. 2.4e-117; Indels 0; Gaps 0;  
Matches 663; Conservative 0; Mismatches 0;

Oy 1 CAACAGACCCCGATCCAGCCCACTTACAGATCTAGTTAGTAAACCTTCAAAAT 60

Db 918 CAACAGACCCCGATCCAGCCCACTTACAGATCTAGTTAGTAAACCTTCAAAAT 977

QY 61 ATATATTTCTTTATGAGGTCACCTGTTACTACGAGAAATGTAATCTCTGTATCAA 120  
Db |||||||  
QY 978 ATATATTTCTTTATGAGGTCACCTGTTACTACGAGAAATGTAATCTCTGTATCAA 1037  
Db |||||||  
QY 121 CTTTATCTCACCATTATATATATATGTTTTCAGGGCCAAATATGATAAAATAAAACT 180  
Db |||||||  
QY 1038 CTTTATCTCACCATTATATATATGTTTTCAGGGCCAAATATGATAAAATAAAACT 1097  
Db |||||||  
QY 161 GAACCTAAGAACCAAGAGATGCAACTTTATTTAAGGATAAAACGTTGATATTTATGTT 240  
Db |||||||  
QY 1098 GAACCTAAGAACCAAGAGATGCAACTTTATTTAAGGATAAAACGTTGATATTTATGTT 1157  
Db |||||||  
QY 241 GTAGATATTTACCATCTCTGTTTATTTATGTAAGAAATGCAAGAGGAGTCATGTTATCTAC 300  
Db |||||||  
QY 1158 GTAGATATTTACCATCTCTGTTTATTTATGTAAGAAATGCAAGAGGAGTCATGTTATCTAC 1217  
Db |||||||  
QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 360  
Db |||||||  
QY 1218 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 1277  
Db |||||||  
QY 361 GTATCAATCGATGGTATCCAAAGCCATCATTTGATATTTGAACAAATAAAAAATGGTA 420  
Db |||||||  
QY 1278 GTATCAATCGATGGTATCCAAAGCCATCATTTGATATTTGAACAAATAAAAAATGGTA 1337  
Db |||||||  
QY 421 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATAAATGAACAACTATAT 480  
Db |||||||  
QY 1338 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATAAATGAACAACTATAT 1397  
Db |||||||  
QY 481 ACTAATGGAACCTTCAATATGAAACTGGATATATAAAGTTTCACTAAGAAATAAAGAA 540  
Db |||||||  
QY 1398 ACTAATGGAACCTTCAATATGAAACTGGATATATAAAGTTTCACTAAGAAATAAAGAA 1457  
Db |||||||  
QY 541 AGTTTGTGTTTCAATTTTTCCTGTAACAGAAATTTACTCAATCTAAATCTTATGATA 600  
Db |||||||  
QY 1458 AGTTTGTGTTTCAATTTTTCCTGTAACAGAAATTTACTCAATCTAAATCTTATGATA 1517  
Db |||||||  
QY 601 TATAAGATATGAACCGTTGACTCAACACAAAGCCAAATGAAAGTCTACCTAACACACC 660  
Db |||||||  
QY 1518 TATAAGATATGAACCGTTGACTCAACACAAAGCCAAATGAAAGTCTACCTAACACACC 1577  
Db |||||||

## RESULT 2

US-09-308-830-12  
; Sequence 12, Application US/09308830  
; Publication No. US20020086813A1  
; GENERAL INFORMATION:  
; APPLICANT: Regents of the University of Minnesota  
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A  
; AND METHODS OF USE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Merchant & Gould P.C.  
; STREET: P.O. Box 2903  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402-0903  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/308,830  
; FILING DATE: 04-Aug-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/22228  
; FILING DATE: 05-DEC-1997

APPLICATION NUMBER: 60/032,930  
FILING DATE: 06-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Skoog, Mark T  
REGISTRATION NUMBER: 40,178  
REFERENCE/DOCKET NUMBER: 600.346USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1851 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 828..1580  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-308-830-12

Query Match 100.0%; Score 663; DB 13; Length 1851;  
Best Local Similarity 100.0%; Pred. No. 2.4e-117;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAACAAGACCCGGATCCAAAGCCAACTTCAAGATCTAGTTTAGTTTAAAAACCTTCAAAT 60  
Db |||||||  
QY 918 CAACAAGACCCGGATCCAAAGCCAACTTCAAGATCTAGTTTAGTTTAAAAACCTTCAAAT 977  
Db |||||||  
QY 61 ATATATTTCTTTATGAGGTCACCTGTTACTACGAGAAATGTAATCTCTGTATCAA 120  
Db |||||||  
QY 978 ATATATTTCTTTATGAGGTCACCTGTTACTACGAGAAATGTAATCTCTGTATCAA 1037  
Db |||||||  
QY 121 CTTTATCTCACCATTATATATATGTTTTCAGGGCCAAATATGATAAAATAAAACT 180  
Db |||||||  
QY 1038 CTTTATCTCACCATTATATATATGTTTTCAGGGCCAAATATGATAAAATAAAACT 1097  
Db |||||||  
QY 181 GAACCTAAGAACCAAGAGATGCAACTTTATTTAAGGATAAAGCTGTTGATATTTATGTT 240  
Db |||||||  
QY 1098 GAACCTAAGAACCAAGAGATGCAACTTTATTTAAGGATAAAGCTGTTGATATTTATGTT 1157  
Db |||||||  
QY 241 GTAGATATTTACCATCTCTGTTTATTTATGTAAGAAATGCAAGAGGAGTCATGTTATCTAC 1217  
Db |||||||  
QY 301 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 360  
Db |||||||  
QY 1218 GGAGGGGTAAACAAATCATGAAGGGAATCATTTAGAAATTCCTTAAAAAGATAGTCGTTAAA 1277  
Db |||||||  
QY 361 GTATCAATCGATGGTATCCAAAGCCATCATTTGATATTTGAACAAATAAAAAATGGTA 420  
Db |||||||  
QY 1278 GTATCAATCGATGGTATCCAAAGCCATCATTTGATATTTGAACAAATAAAAAATGGTA 1337  
Db |||||||  
QY 421 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATAAATGAACAACTATAT 480  
Db |||||||  
QY 1338 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATAAATGAACAACTATAT 1397  
Db |||||||  
QY 481 ACTAATGGAACCTTCAATATGAAACTGGATATATAAAGTTTCACTAAGAAATAAAGAA 540  
Db |||||||  
QY 1398 ACTAATGGAACCTTCAATATGAAACTGGATATATAAAGTTTCACTAAGAAATAAAGAA 1457  
Db |||||||  
QY 541 AGTTTGTGTTTCAATTTTTCCTGTAACAGAAATTTACTCAATCTAAATCTTATGATA 600  
Db |||||||  
QY 1458 AGTTTGTGTTTCAATTTTTCCTGTAACAGAAATTTACTCAATCTAAATCTTATGATA 1517  
Db |||||||  
QY 601 TATAAGATATGAACCGTTGACTCAACACAAAGCCAAATGAAAGTCTACCTAACACACC 660  
Db |||||||  
QY 1518 TATAAGATATGAACCGTTGACTCAACACAAAGCCAAATGAAAGTCTACCTAACACACC 1577  
Db |||||||  
QY 661 AAG 663

Db 1578 AAG 1580

RESULT 3

US-09-452-599-33

; Sequence 33, Application US/09452599

; Patent No. US20020055101A1

; GENERAL INFORMATION:

; APPLICANT: Bergeron, Michel G.

; APPLICANT: Ouellette, Marc

; APPLICANT: Roy, Paul H.

; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers

; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial

; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical

; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro

; FILE REFERENCE: 12287.31

; CURRENT APPLICATION NUMBER: US/09/452,599

; CURRENT FILING DATE: 1999-12-01

; PRIOR FILING DATE: 1995-09-24

; PRIOR APPLICATION NUMBER: 08/526,840

; PRIOR FILING DATE: 1999-09-24

; PRIOR FILING DATE: 08/304,732

; PRIOR FILING DATE: 1999-09-12

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 33

; LENGTH: 1837

; TYPE: DNA

; ORGANISM: Streptococcus pyogenes

US-09-452-599-33

Query Match 99.8%; Score 661.4; DB 9; Length 1837;

Best Local Similarity 99.8%; Pred. No. 4.9e-117;

Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACAAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 60

Db 904 CAACAAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 963

Qy 61 ATATATTTCTTTATGAGGGTGACCTGTTACTCACGAGATGTAATCTGTTGATCAA 120

Db 964 ATATATTTCTTTATGAGGGTGACCTGTTACTCACGAGATGTAATCTGTTGATCAA 1023

Qy 121 CTTTATCTCACCATTAAATATAATGTTTACGGCCAAATTAATGATAATTAATAACT 180

Db 1024 CTTTATCTCACCATTAAATATAATGTTTACGGCCAAATTAATGATAATTAATAACT 1083

Qy 181 GAACCTTAAGAACCAAGAGATGGCAACTTTATTAAGGATAAAAAACGTTGATTTATGGT 240

Db 1084 GAACCTTAAGAACCAAGAGATGGCAACTTTATTAAGGATAAAAAACGTTGATTTATGGT 1143

Qy 241 GTAGAATATTACCATCTCTGTTATTTATGTAAGGATGCAAGAGAGTGATCTAC 300

Db 1144 GTAGAATATTACCATCTCTGTTATTTATGTAAGGATGCAAGAGAGTGATCTAC 1203

Qy 301 GGAGGGGTAAACAATCATGAGGGAATCATTTAGAAATTCCTAAAGATAGTCTGTTAA 360

Db 1204 GGAGGGGTAAACAATCATGAGGGAATCATTTAGAAATTCCTAAAGATAGTCTGTTAA 1263

Qy 361 GTATCAATTCGATGTTATCCAAAGCCTATCTTATGATTTGAAACAAATAAAAAATGGTA 420

Db 1264 GTATCAATTCGATGTTATCCAAAGCCTATCTTATGATTTGAAACAAATAAAAAATGGTA 1323

Qy 421 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAAATCTTACAGATAATAAGCAACTATAT 480

Db 1324 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAAATCTTACAGATAATAAGCAACTATAT 1383

Qy 481 ACTAATGGACCTCTTAATATCAACTGGATATATTAAGTTTCACTACCTAAGAAATAAGAA 540

Db 1384 ACTAATGGACCTCTTAATATCAACTGGATATATTAAGTTTCACTACCTAAGAAATAAGAA 1443

Qy 541 AGTTTGGTTGGTTGATTTTCCCTCGAACCAAGATTTACTCAATCTTAATATCTTATGATA 600

Db 1444 AGTTTGGTTGGTTGATTTTCCCTCGAACCAAGATTTACTCAATCTTATGATA 1503

Qy 601 TATAAGATATGAAACGCTTACTCAACAACAGCCAAATTTGAAGTCTACTTACCAACC 660

Db 1504 TATAAGATATGAAACGCTTACTCAACAACAGCCAAATTTGAAGTCTACTTACCAACC 1563

Qy 661 AAG 663

Db 1564 AAG 1566

RESULT 4

US-10-121-120-33

; Sequence 33, Application US/10121120

; Publication No. US20030180733A1

; GENERAL INFORMATION:

; APPLICANT: Bergeron, Michel G.

; APPLICANT: Ouellette, Marc

; APPLICANT: Roy, Paul H.

; TITLE OF INVENTION: Specific and Universal Probes and Amplification

; TITLE OF INVENTION: Primers

; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial

; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical

; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro

; FILE REFERENCE: 12287.31

; CURRENT APPLICATION NUMBER: US/10/121,120

; CURRENT FILING DATE: 2002-04-11

; PRIOR FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: 08/452,599

; PRIOR FILING DATE: 1999-12-01

; PRIOR FILING DATE: 08/304,732

; PRIOR FILING DATE: 1994-09-12

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 33

; LENGTH: 1837

; TYPE: DNA

; ORGANISM: Streptococcus pyogenes

US-10-121-120-33

Query Match 99.8%; Score 661.4; DB 15; Length 1837;

Best Local Similarity 99.8%; Pred. No. 4.9e-117;

Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACAAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 60

Db 904 CAACAAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 963

Qy 61 ATATATTTCTTTATGAGGGTGACCTGTTACTCACGAGATGTAATCTGTTGATCAA 120

Db 964 ATATATTTCTTTATGAGGGTGACCTGTTACTCACGAGATGTAATCTGTTGATCAA 1023

Qy 121 CTTTATCTCACCATTAAATATAATGTTTACGGCCAAATTAATGATAATTAATAACT 180

Db 1024 CTTTATCTCACCATTAAATATAATGTTTACGGCCAAATTAATGATAATTAATAACT 1083

Qy 181 GAACCTTAAGAACCAAGAGATGGCAACTTTATTAAGGATAAAAAACGTTGATTTATGGT 240

Db 1084 GAACCTTAAGAACCAAGAGATGGCAACTTTATTAAGGATAAAAAACGTTGATTTATGGT 1143

Qy 241 GTAGAATATTACCATCTCTGTTATTTATGTAAGGATGCAAGAGAGTGATCTAC 300

Db 1144 GTAGAATATTACCATCTCTGTTATTTATGTAAGGATGCAAGAGAGTGATCTAC 1203

Qy 301 GGAGGGGTAAACAATCATGAGGGAATCATTTAGAAATTCCTAAAGATAGTCTGTTAA 360

Db 1204 GGAGGGGTAAACAATCATGAGGGAATCATTTAGAAATTCCTAAAGATAGTCTGTTAA 1263

Qy 361 GTATCAATTCGATGTTATCCAAAGCCTATCTTATGATTTGAAACAAATAAAAAATGGTA 420

Db 1264 GTATCAATTCGATGTTATCCAAAGCCTATCTTATGATTTGAAACAAATAAAAAATGGTA 1323

Qy 421 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAAATCTTACAGATAATAAGCAACTATAT 480

Db 1324 ACTGCTCAAGAAATAGACTATAAAGTTAGAAAAATCTTACAGATAATAAGCAACTATAT 1383

Qy 481 ACTAATGGACCTCTTAATATCAACTGGATATATTAAGTTTCACTACCTAAGAAATAAGAA 540

Db 1384 ACTAATGGACCTCTTAATATCAACTGGATATATTAAGTTTCACTACCTAAGAAATAAGAA 1443

Qy 541 AGTTTGGTTGGTTGATTTTCCCTCGAACCAAGATTTACTCAATCTTAATATCTTATGATA 600

Db 1444 AGTTTGGTTGGTTGATTTTCCCTCGAACCAAGATTTACTCAATCTTATGATA 1503

Db 1324 ACTGCTCAAGATTAGACTATATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATAT 1383  
QY 481 ACTAATGGACCTTCTAATATATGAAGCTGATATATAAGTTTCATACCTTAAGAAATAAGAA 540  
Db 1384 ACTAATGGACCTTCTAATATATGAAGCTGATATATAAAGTTTCATACCTTAAGAAATAAGAA 1443  
QY 541 AGTTTTTGTTGTTGATTTTTTCCCTGAAACAGAAATTTACTCAATCTAAATATCTTTATGATA 600  
Db 1444 AGTTTTTGTTGTTGATTTTTTCCCTGAAACAGAAATTTACTCAATCTAAATATCTTTATGATA 1503  
QY 601 TATAAGATAATGAACGCTTGACTCAAAACAAGCCAAATTTGAAGTCTTACCTAACCAACC 660  
Db 1504 TATAAGATAATGAACGCTTGACTCAAAACAAGCCAAATTTGAAGTCTTACCTAACCAACC 1563  
QY 661 AAG 663  
Db 1564 AAG 1566

## RESULT 5

US-08-882-431-15  
; Sequence 15, Application US/08882431  
; Publication No. US2003009015A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Ulrich,  
; APPLICANT: Mark A. Olson  
; APPLICANT: Sina Bavari  
; TITLE OF INVENTION: Bacterial Superantigen  
; TITLE OF INVENTION: Vaccines  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John Moran  
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)  
; CITY: FORT DETRICK  
; STATE: MARYLAND  
; COUNTRY: USA  
; ZIP: 21702-5012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.5  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/882,431  
; FILING DATE: June 25, 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Moran, John  
; REGISTRATION NUMBER: 26,313  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 619-2065  
; TELEFAX: (301) 619-7714  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1837  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: DNA  
US-08-882-431-15

Query Match 99.3%; Score 658.2; DB 8; Length 1837;  
Best Local Similarity 99.5%; Pred. No. 2e-116;  
Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTTACGTTAAACCTTCAAAAT 60  
Db 904 CAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTTACGTTAAACCTTCAAAAT 963

QY 61 ATATATTTCTTTATGAGGTTGACCTGTACTACAGAAATGTGAAATCTCTGATCAA 120  
Db 964 ATATATTTCTTTATGAGGTTGACCTGTACTACAGAAATGTGAAATCTCTGATCAA 1023  
QY 121 CTTTATCTCAACATTTAATATATATGTTTCAGGGCCAAATATGATAAATAAACT 180  
Db 1024 CTTAGATCTCAGATTTAATATATATGTTTCAGGGCCAAATATGATAAATAAACT 1083  
QY 181 GAACCTTAAGACCAAGAGATGGCACTTTATTTAAGGATATAAAGCTTTGATATTTATGCT 240  
Db 1084 GAACCTTAAGACCAAGAGATGGCACTTTATTTAAGGATATAAAGCTTTGATATTTATGCT 1143  
QY 241 GTAGAATATACCACTCTCTGTTTATTTATGTAAGATGAGAGAGGAGTGTATCTAC 300  
Db 1144 GTAGATATATACCATCTCTGTTTATTTATGTAAGATGAGAGAGGAGTGTATCTAC 1203  
QY 301 GGAGGGTAAACAAATCATGAAGGAATCATTTAGAAATTCCTTAAAGATAGTCTGTAAA 360  
Db 1204 GGAGGGTAAACAAATCATGAAGGAATCATTTAGAAATTCCTTAAAGATAGTCTGTAAA 1263  
QY 361 GTATCAATCGATGGTATCCAAAGCCCTATCTTGTATTTGAACAAATAAATAAATGGTA 420  
Db 1264 GTATCAATCGATGGTATCCAAAGCCCTATCTTGTATTTGAACAAATAAATAAATGGTA 1323  
QY 421 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATAT 480  
Db 1324 ACTGCTCAAGATTTAGACTATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATAT 1383  
QY 481 ACTAATGGACCTTCTAATATATGAAGCTGATATATAAGTTTCATACCTTAAGAAATAAGAA 540  
Db 1384 ACTAATGGACCTTCTAATATATGAAGCTGATATATAAGTTTCATACCTTAAGAAATAAGAA 1443  
QY 541 AGTTTTTGTTGTTGATTTTTTCCCTGAAACAGAAATTTACTCAATCTAAATATCTTTATGATA 600  
Db 1444 AGTTTTTGTTGTTGATTTTTTCCCTGAAACAGAAATTTACTCAATCTAAATATCTTTATGATA 1503  
QY 601 TATAAGATAATGAACGCTTGACTCAAAACAAGCCAAATTTGAAGTCTTACCTAACCAACC 660  
Db 1504 TATAAGATAATGAACGCTTGACTCAAAACAAGCCAAATTTGAAGTCTTACCTAACCAACC 1563  
QY 661 AAG 663  
Db 1564 AAG 1566

## RESULT 6

US-10-002-784A-15  
; Sequence 15, Application US/10002784A  
; Publication No. US20030036644A1  
; GENERAL INFORMATION:  
; /33  
; APPLICANT: Ulrich, Robert G.  
; TITLE OF INVENTION: Bacterial Superantigen Vaccines  
; FILE REFERENCE: 003/233/SAP  
; CURRENT APPLICATION NUMBER: US/10/002,784A  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776  
; PRIOR FILING DATE: 97-06-25; 98-09-01  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 15  
; LENGTH: 1837  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant  
US-10-002-784A-15

Query Match 99.0%; Score 656.6; DB 15; Length 1837;  
Best Local Similarity 99.4%; Pred. No. 4.1e-116;  
Matches 659; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTTACGTTAAACCTTCAAAAT 60



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Db 904 CAACAGACCCCGATCCAGCACTTCACAGATCTAGTTTGTATTAATAACCTTCAAAAT 963
Qy 61 ATATATTTCTTTATAGGGGTGACCCCTGTTACTCACGAGAAATGTGAAATCTGTTGATCAA 120
Db 964 ATATATTTCTTTATAGGGGTGACCCCTGTTACTCACGAGAAATGTGAAATCTGTTGATCAA 1023
Qy 121 CTTTATCTCACCATTAAATATAATAGTTTTCAGGGCCAAATTAATGATAAATTAATAACT 180
Db 1024 CTTAGATCTCAGGATTTAAATATAATAGTTTTCAGGGCCAAATTAATGATAAATTAATAACT 1083
Qy 181 GAACTTAAGAACCAAGAGATGCGCACTTTATTTAAGGATAAATAAGTTTGATTAATTTATGGT 240
Db 1084 GAACTTAAGAACCAAGAGATGCGCACTTTATTTAAGGATAAATAAGTTTGATTAATTTATGGT 1143
Qy 241 GTAGAATATTACCATCTCTGTTATTTATGTGAAATGCGAAGAGGATGCGATGATCTAC 300
Db 1144 GTAGAATATTACCATCTCTGTTATTTATGTGAAATGCGAAGAGGATGCGATGATCTAC 1203
Qy 301 GGAGGGGTAAACAATCATGAGGGNAATCAATTAGAAATTCCTAATAAGATAGTCTTAAA 360
Db 1204 GGAGGGGTAAACAATCATGAGGGNAATCAATTAGAAATTCCTAATAAGATAGTCTTAAA 1263
Qy 361 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATATAAATAATGGTA 420
Db 1264 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATATAAATAATGGTA 1323
Qy 421 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATTAACCACTATAT 480
Db 1324 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATTAACCACTATAT 1383
Qy 481 ACTAATGACCTTCTAAATATGAACCTGGATATATTAAGTTTCACTACCTAAGAAATAGAA 540
Db 1384 ACTAATGACCTTCTAAATATGAACCTGGATATATTAAGTTTCACTACCTAAGAAATAGAA 1443
Qy 541 AGTTTTCGTTGATTTTTCCTTGAACCAAGATTTTCTCAATCTAATATCTTATGATA 600
Db 1444 AGTTTTCGTTGATTTTTCCTTGAACCAAGATTTTCTCAATCTAATATCTTATGATA 1503
Qy 601 TATAAGATAATGAACCTGTTGACTCAACCAAGCAAAATGAAGTCTACCTAACCAACC 660
Db 1504 TATAAGATAATGAACCTGTTGACTCAACCAAGCAAAATGAAGTCTACCTAACCAACC 1563
Qy 661 AAG 663
Db 1564 AAG 1566
```

## RESULT 7

US-10-002-784A-23  
; Sequence 23, Application US/10002784A  
; Publication No. US2003003664A1  
; GENERAL INFORMATION:

APPLICANT: Ulrich, Robert G.  
; TITLE OF INVENTION: Bacterial Superantigen Vaccines  
; FILE REFERENCE: 003/233/SAP  
; CURRENT APPLICATION NUMBER: US/10/002,784A  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776  
; PRIOR FILING DATE: 97-06-25; 98-09-01  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 23  
; LENGTH: 1419  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: mutant SpeA/mutant SpeB fusion  
US-10-002-784A-23

Query Match 98.3%; Score 651.8; DB 15; Length 1419;  
Best Local Similarity 98.9%; Pred. No. 3.1e-115;

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Matches 656; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CAACAGACCCCGATCCAGCACTTCACAGATCTAGTTTGTATTAATAACCTTCAAAAT 60
Db 4 CAACAGACCCCGATCCAGCACTTCACAGATCTAGTTTGTATTAATAACCTTCAAAAT 63
Qy 61 ATATATTTCTTTATAGGGGTGACCCCTGTTACTCACGAGAAATGTGAAATCTGTTGATCAA 120
Db 64 ATATATTTCTTTATAGGGGTGACCCCTGTTACTCACGAGAAATGTGAAATCTGTTGATCAA 123
Qy 121 CTTTATCTCACCATTAAATATAATAGTTTTCAGGGCCAAATTAATGATAAATTAATAACT 180
Db 124 CTTGATCTCAGGATTTAAATATAATAGTTTTCAGGGCCAAATTAATGATAAATTAATAACT 183
Qy 181 GAACTTAAGAACCAAGAGATGCGCACTTTATTTAAGGATAAATAAGTTTGATTAATTTATGGT 240
Db 184 GAACTTAAGAACCAAGAGATGCGCACTTTATTTAAGGATAAATAAGTTTGATTAATTTATGGT 243
Qy 241 GTAGAATATTACCATCTCTGTTATTTATGTGAAATGCGAAGAGGATGCGATGATCTAC 300
Db 244 GTAGAATATTACCATCTCTGTTATTTATGTGAAATGCGAAGAGGATGCGATGATCTAC 303
Qy 301 GGAGGGGTAAACAATCATGAGGGNAATCAATTAGAAATTCCTAATAAGATAGTCTTAAA 360
Db 304 GGAGGGGTAAACAATCATGAGGGNAATCAATTAGAAATTCCTAATAAGATAGTCTTAAA 363
Qy 361 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATATAAATAATGGTA 420
Db 364 GTATCAATCGATGGTATCCAAAGCCTATCATTTGATATTGAAACAAATATAAATAATGGTA 423
Qy 421 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATTAACCACTATAT 480
Db 424 ACTGCTCAAGAAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATTAACCACTATAT 483
Qy 481 ACTAATGACCTTCTAAATATGAACCTGGATATATTAAGTTTCACTACCTAAGAAATAGAA 540
Db 484 ACTAATGACCTTCTAAATATGAACCTGGATATATTAAGTTTCACTACCTAAGAAATAGAA 543
Qy 541 AGTTTTCGTTGATTTTTCCTTGAACCAAGATTTTCTCAATCTAATATCTTATGATA 600
Db 544 AGTTTTCGTTGATTTTTCCTTGAACCAAGATTTTCTCAATCTAATATCTTATGATA 603
Qy 601 TATAAGATAATGAACCTGTTGACTCAACCAAGCAAAATGAAGTCTACCTAACCAACC 660
Db 604 TATAAGATAATGAACCTGTTGACTCAACCAAGCAAAATGAAGTCTACCTAACCAACC 663
Qy 661 AAG 663
Db 664 AAG 666
```

## RESULT 8

US-09-870-759-19  
; Sequence 19, Application US/09870759  
; Patent No. US20020177551A1  
; GENERAL INFORMATION:

APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 870759  
; CURRENT APPLICATION NUMBER: US/09/870,759  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: US 60/208,128  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 1031  
; TYPE: DNA  
; ORGANISM: Streptococcus pyogenes  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (79)..(831)  
; OTHER INFORMATION:

US-09-870-759-19

Query Match 87.9%; Score 582.6; DB 9; Length 1031;  
Best Local Similarity 97.1%; Pred. No. 5e-102;  
Matches 636; Conservative 0; Mismatches 14; Indels 5; Gaps 4;

QY 10 CCCGATCCAAAGCCAACTTCACAGATCTAGTTTAGTTTAAACCTTCAAAATATATATTTT 69  
DB 178 CCCAAGCCAGCCAACTTACAAAGATCTAATTTAGTT-AAAACCTTCAAAATATATATTTT 236

QY 70 CTTTATGAGGGTGACCCCT-GTTACTCACGAGAAATGTGAAATCTGTGTGATCAACTTTATC 128  
DB 237 CTTTATGAGGGTGACCCCTGTTACTCACGAGAAATGTGAAATCTGTGTGATCAACTTTATC 296

QY 129 TCACCAATTTAATATATATGTTTCAGGGCCAAATATGATAATTAATAACTGAACCTTAA 188  
DB 297 ACACGATTTAATATATATGTTTCAGGGCCAAATATGATAATTAATAACTGAACCTTAA 356

QY 189 GAACCAAGAGATGGCAACTTTATTTAAGGATAAAACGTTGTATTTATGGTGTAGAAATA 248  
DB 357 GAACCAAGAGATGGCAACTTTATTTAAGGATAAAACGTTGTATTTATGGTGTAGAAATA 416

QY 249 TTACCATCTCTGTTATTTATGTGAAAATCGAAGAGAGTGATGATCTACGGAGGGGT 308  
DB 417 TTACCATCTCTGTTATTTATGTGAAAATCGAAGAGAGTGATGATCTCTACGGAGGGGT 476

QY 309 AACCAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 368  
DB 477 AACCAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 536

QY 369 CGATGGTATCCAAAGCCCTATCATTTGATATGAAACAAATAAAAAATGGTAACCTGCTCA 428  
DB 537 CGATGGTATCCAAAGCCCTATCATTTGATATGAAACAAATAAAAAATGGTAACCTGCTCA 594

QY 429 AGAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATATACTAATGG 488  
DB 595 AGAATTAG-CTATACAGTTAGAAAATATCTTACAGATAATAAGCAACTATATACTAATGG 653

QY 489 ACCTTCTAAATATGAACCTGGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGG 548  
DB 654 ACCTTCTAAATATGAACCTGGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGG 713

QY 549 GTTTCATTTTCCCTGAACCAAGAAATTTACTCAATCTAAATCTTATGATATATAAAGA 608  
DB 714 GTTTCATTTTCCCTGAACCAAGAAATTTACTCAATCTAAATCTTATGATATATAAAGA 773

QY 609 TAATGAACCGTTGACTCAACACAGCAAGCAAAATTTGAAGTCTACCTAACCAACCAAG 663  
DB 774 TAATGAACCGTTGACTCAACACAGCAAGCAAAATTTGAAGTCTACCTAACCAACCAAG 828

RESULT 9

US-09-751-708A-19  
; Sequence 19, Application US/09751708A  
; Publication No. US20030157113A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 751708  
; CURRENT APPLICATION NUMBER: US/09/751,708A  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 60/173,371  
; PRIOR FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 1031  
; TYPE: DNA  
; ORGANISM: Streptococcus pyogenes  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (79)..(831)  
; OTHER INFORMATION:

US-09-751-708A-19

Query Match 87.9%; Score 582.6; DB 10; Length 1031;  
Best Local Similarity 97.1%; Pred. No. 5e-102;  
Matches 636; Conservative 0; Mismatches 14; Indels 5; Gaps 4;

QY 10 CCCGATCCAAAGCCAACTTCACAGATCTAGTTTAGTTTAAACCTTCAAAATATATATTTT 69  
DB 178 CCCAAGCCAGCCAACTTACAAAGATCTAATTTAGTT-AAAACCTTCAAAATATATATTTT 236

QY 70 CTTTATGAGGGTGACCCCT-GTTACTCACGAGAAATGTGAAATCTGTGTGATCAACTTTATC 128  
DB 237 CTTTATGAGGGTGACCCCTGTTACTCACGAGAAATGTGAAATCTGTGTGATCAACTTTATC 296

QY 129 TCACCAATTTAATATATATGTTTCAGGGCCAAATATGATAATTAATAACTGAACCTTAA 188  
DB 297 ACACGATTTAATATATATGTTTCAGGGCCAAATATGATAATTAATAACTGAACCTTAA 356

QY 189 GAACCAAGAGATGGCAACTTTATTTAAGGATAAAACGTTGTATTTATGGTGTAGAAATA 248  
DB 357 GAACCAAGAGATGGCAACTTTATTTAAGGATAAAACGTTGTATTTATGGTGTAGAAATA 416

QY 249 TTACCATCTCTGTTATTTATGTGAAAATCGAAGAGAGTGATGATCTACGGAGGGGT 308  
DB 417 TTACCATCTCTGTTATTTATGTGAAAATCGAAGAGAGTGATGATCTCTACGGAGGGGT 476

QY 309 AACCAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 368  
DB 477 AACCAATCATGAAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCGTTAAAGTATCAAT 536

QY 369 CGATGGTATCCAAAGCCCTATCATTTGATATGAAACAAATAAAAAATGGTAACCTGCTCA 428  
DB 537 CGATGGTATCCAAAGCCCTATCATTTGATATGAAACAAATAAAAAATGGTAACCTGCTCA 594

QY 429 AGAATTAGACTATAAAGTTAGAAAATATCTTACAGATAATAAGCAACTATATACTAATGG 488  
DB 595 AGAATTAG-CTATACAGTTAGAAAATATCTTACAGATAATAAGCAACTATATACTAATGG 653

QY 489 ACCTTCTAAATATGAACCTGGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGG 548  
DB 654 ACCTTCTAAATATGAACCTGGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGG 713

QY 549 GTTTCATTTTCCCTGAACCAAGAAATTTACTCAATCTAAATCTTATGATATATAAAGA 608  
DB 714 GTTTCATTTTCCCTGAACCAAGAAATTTACTCAATCTAAATCTTATGATATATAAAGA 773

QY 609 TAATGAACCGTTGACTCAACACAGCAAGCAAAATTTGAAGTCTACCTAACCAACCAAG 663  
DB 774 TAATGAACCGTTGACTCAACACAGCAAGCAAAATTTGAAGTCTACCTAACCAACCAAG 828

RESULT 10

US-09-870-759-11  
; Sequence 11, Application US/09870759  
; Patent No. US20020177551A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 870759  
; CURRENT APPLICATION NUMBER: US/09/870,759  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: US 60/208,128  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 1095  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (118)..(918)  
; OTHER INFORMATION:

US-09-870-759-11

Query Match 25.2%; Score 167.4; DB 9; Length 1095;  
Best Local Similarity 59.0%; Pred. No. 1.7e-22;  
Matches 382; Conservative 0; Mismatches 226; Indels 39; Gaps 4;

QY 56 AAAATATATATTTCTTTATGAGGGTGACCTGTTACTCAGGAGAAATGTGAAATCTCTTG 115  
DB 263 AAAATATGAAAGTTTTATATGATGATCATTTATGATCAGCAACTAAAAGTTAAGTCTGTAG 322

QY 116 ATCAACTTTTATCTCACCATTATATATATATATGTTTCAGG-----GCCAAATATG 166  
DB 323 ATAAATTTTGGCACATGATTTAATTTATACATTAGTGATAAAAAACTGAAAAATATG 382

QY 167 ATAAATTAATAACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATAAAAAAG 226  
DB 383 ACAAAGTGAACACAGAGTTTATTAATGAAGGTTTAGCAAAAGAGTACAAAAGATGAAGTAG 442

QY 227 TTGATATTTATGTTGTAGATATATACCATCTCTGTTATTTAT----- 268  
DB 443 TTGATGTATGGATCAAAATTTACTGTAAACTGCTATTTTTTCATCCAAAGATATGTAG 502

QY 269 GTGAAAATGCAGAAAGAGTGATGATCTACGGAGGGGTAAACAAATCATGAAGGGATC 328  
DB 503 GTAAAGTTACAGGTGGCAAACTTGTATGTATGGAGGATTAACAAACATGAAGGAAACC 562

QY 329 ATTTAGAAATTCCTA-----AAAAGATAGTCGTTAAAGTATCAATCGATGGTATCCAAA 382  
DB 563 ACTTTGATAATGGGAACCTTACAAAATGTACTTTATAAGAGTTTATGAAAATAAAAAAGAAACA 622

QY 383 GCCTATCATTTGATTTGAACAAATAAAAAATGTTAACTGCTCAAGAAATTAAGACTATA 442  
DB 623 CAATTTCTTTTGAAGTGCRAACTGATGAAGAAAGTGAACAGCTCAAGAACTAGACATA 682

QY 443 AAGTTAGAAATATCTTTACAGATAATAAGCAACTATATATACTAAATGGACCTTCTAAATATG 502  
DB 683 AAGCTAGAAATTTTAAATTAATAAAAAATTTGTATGAGTTTAAACAGTTCCACCATATG 742

QY 503 AAATCGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGGTTGATTTTTCCTCC 562  
DB 743 AAACAGGATATATAAATTTATTGAAAATAACGGCAATACCTTTTGGTATGATATGTC 802

QY 563 CTGAACACAG-----AATTTACTCAATCTAAATATCTTATGATATATAAGATATGAAA 616  
DB 803 CTGCACACAGCGATAGTTTGACCAATCTAAATTTAATGATGTACACGCAATATAA 862

QY 617 CGTTTGACTCAACACACAGCCAAATTTGAAGTCTACCTAACCAACCAAG 663  
DB 863 CGGTTGATTTCTAAAAGTGTGAAGATAGAGTCCACCTTACAAACAAG 909

RESULT 11  
US-09-751-708A-11  
; Sequence 11, Application US/09751708A  
; Publication No. US20030157113A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 751708  
; CURRENT APPLICATION NUMBER: US/09/751,708A  
; PRIORITY FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 60/173,371  
; PRIORITY FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 1095  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (118)..(918)  
; OTHER INFORMATION:

US-09-751-708A-11

Query Match 25.2%; Score 167.4; DB 10; Length 1095;  
Best Local Similarity 59.0%; Pred. No. 1.7e-22;  
Matches 382; Conservative 0; Mismatches 226; Indels 39; Gaps 4;

QY 56 AAAATATATATTTCTTTATGAGGGTGACCTGTTACTCAGGAGAAATGTGAAATCTCTTG 115  
DB 263 AAAATATGAAAGTTTTATATGATGATCATTTATGATCAGCAACTAAAAGTTAAGTCTGTAG 322

QY 116 ATCAACTTTTATCTCACCATTATATATATATATGTTTCAGG-----GCCAAATATG 166  
DB 323 ATAAATTTTGGCACATGATTTAATTTATACATTAGTGATAAAAAACTGAAAAATATG 382

QY 167 ATAAATTAATAACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATAAAAAAG 226  
DB 383 ACAAAGTGAACACAGAGTTTATTAATGAAGGTTTAGCAAAAGAGTACAAAAGATGAAGTAG 442

QY 227 TTGATATTTATGTTGTAGATATATACCATCTCTGTTATTTAT----- 268  
DB 443 TTGATGTATGGATCAAAATTTACTGTAAACTGCTATTTTTTCATCCAAAGATATGTAG 502

QY 269 GTGAAAATGCAGAAAGAGTGATGATCTACGGAGGGGTAAACAAATCATGAAGGGATC 328  
DB 503 GTAAAGTTACAGGTGGCAAACTTGTATGTATGGAGGATTAACAAACATGAAGGAAACC 562

QY 329 ATTTAGAAATTCCTA-----AAAAGATAGTCGTTAAAGTATCAATCGATGGTATCCAAA 382  
DB 563 ACTTTGATAATGGGAACCTTACAAAATGTACTTTATAAGAGTTTATGAAAATAAAAAAGAAACA 622

QY 383 GCCTATCATTTGATTTGAACAAATAAAAAATGTTAACTGCTCAAGAAATTAAGACTATA 442  
DB 623 CAATTTCTTTTGAAGTGCRAACTGATGAAGAAAGTGAACAGCTCAAGAACTAGACATA 682

QY 443 AAGTTAGAAATATCTTTACAGATAATAAGCAACTATATATACTAAATGGACCTTCTAAATATG 502  
DB 683 AAGCTAGAAATTTTAAATTAATAAAAAATTTGTATGAGTTTAAACAGTTCCACCATATG 742

QY 503 AAATCGATATATAAAGTTCTACCTAAGATAAAGAAAGTTTGGTTGATTTTTCCTCC 562  
DB 743 AAACAGGATATATAAATTTATTGAAAATAACGGCAATACCTTTTGGTATGATATGTC 802

QY 563 CTGAACACAG-----AATTTACTCAATCTAAATATCTTATGATATATAAGATATGAAA 616  
DB 803 CTGCACACAGCGATAGTTTGACCAATCTAAATTTAATGATGTACACGCAATATAA 862

QY 617 CGTTTGACTCAACACACAGCCAAATTTGAAGTCTACCTAACCAACCAAG 663  
DB 863 CGGTTGATTTCTAAAAGTGTGAAGATAGAGTCCACCTTACAAACAAG 909

RESULT 12  
US-10-354-948-1  
; Sequence 1, Application US/10354948  
; Publication No. US20030202962A1  
; GENERAL INFORMATION:  
; APPLICANT: Dow, Steve W.  
; Elmslie, Robyn E.  
; Potter, Terence A.  
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, Suite 3500  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.A.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25



US-09-751-708A-1  
; Sequence 1, Application US/09751708A  
; Publication No. US20030157113A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 751708  
; CURRENT APPLICATION NUMBER: US/09/751,708A  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 60/173,371  
; PRIOR FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 801  
; TYPE: DNA  
; ORGANISM: Staphylococcus sp.  
US-09-751-708A-1

```
Query Match      25.2%; Score 166.8; DB 10; Length 801;
Best Local Similarity 59.1%; Pred. No. 2e-22; Indels 45; Gaps 4;
Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;

QY 56 AAAATATATATATTTCTTTATGAGGGTGACCCCTGTTACTCAGGAGATGTGAAATCTGTG 115
Db 146 AAAATATGAAAGTTTGTATGATGATAATCAIGTATCAGCAATAAAGCTTAAATCTATAG 205

QY 116 ATCAACTTTTATCTCACCATTATATATATATATGTTTCAGGGCCA-----AATTATG 166
Db 206 ATCAATTTCTTACTTTTGACTTAAATATATCTTATTAAGGACACTAAGTTAGGGAAATTATG 265

QY 167 ATAAATTAATAAAGTCAACTTAAGAACCAAGAGATGGCAACTTTATTAAGGATAAAACG 226
Db 266 ATATGTTTCGAGTCGAATTTTAAACAAGATTTAGCTGATAAATACAAAGATAAATACG 325

QY 227 TTGATATTTATGGTGTAGAATATTACCATCTCTGTTATTTATGTAATA-----AATTATG 275
Db 326 TAGATGTTGTTGGAGCTAATTTATTTATCAATGTTATTTTCTTAAACAAACGATGATA 385

QY 276 -----TGCAGAAAGGAGTGATGATCTACGAGGGGTACAAATCATG 319
Db 386 TTAATTCGCATCAAACTGACAAACGAAACCTTGTATGTTGTTGTTAACTGAGCATA 445

QY 320 AAGGAATCAITTTAGAAATTCCTTAAAGAGATAGTCGTTTAAAGTATCAATCGATGGTATCC 379
Db 446 ATGNAACCAATTAGATAAATATAGAGATATTACTGTTCCGGGTATTTGAAGATGTAATA 505

QY 380 AAAGCCTATCATTTGATATTGAAACAAATAAAAAAATGTTAACTGCTCAAGAAATTAGACT 439
Db 506 ATTTATTTATCTTTTGACGTACAACTAATAAGAAAAAGGTGACTGCTCAAGAAATTAGATT 565

QY 440 ATAAAGTTAGAAATATCTTACAGTATATAGCAACTATATACTAATGACCTTCTAAAT 499
Db 566 ACCTAATCTGTCATTTTGTGAAAAATAAAAACTCTATGAATTTTAAACACTCGCCTT 625

QY 500 ATGAACTGGATATATAAAGTTTCATACCTAAGATAAAGAAAGTTTTTGGTTTGGATTTT 559
Db 626 ATGAAACGGGATATATTAATTTATA---GAAATGAGAAATAGCTTTTGGTATGACATGA 682

QY 560 TCCCTGAACCCAG-----AATTACTCAATCTAAATCTTTATGATATATAAAGATATG 613
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RESULT 15

US-09-870-759-2  
; Sequence 2, Application US/09870759  
; Patent No. US2002017551A1  
; GENERAL INFORMATION:

; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 870759  
; CURRENT APPLICATION NUMBER: US/09/870,759  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: US 60/208,128  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 886  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-870-759-2

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Query Match      25.2%; Score 166.8; DB 9; Length 886;
Best Local Similarity 59.1%; Pred. No. 2e-22; Indels 45; Gaps 4;
Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;

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QY 116 ATCAACTTTTATCTCACCATTATATATATATATGTTTCAGGGCCA-----AATTATG 166
Db 248 ATCAATTTCTTACTTTTGACTTAAATATATCTTATTAAGGACACTAAGTTAGGGAAATTATG 307

QY 167 ATAAATTAATAAAGTCAACTTAAGAACCAAGAGATGGCAACTTTATTAAGGATAAAACG 226
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QY 276 -----TGCAGAAAGGAGTGATGATCTACGAGGGGTACAAATCATG 319
Db 428 TTAATTCGCATCAAACTGACAAACGAAACCTTGTATGTTGTTGTTAACTGAGCATA 487

QY 320 AAGGAATCAITTTAGAAATTCCTTAAAGAGATAGTCGTTTAAAGTATCAATCGATGGTATCC 379
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Search completed: September 3, 2004, 20:03:05  
Job time : 426 secs

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